GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: September 3, 2005, 07:35:04 ; Search time 1164 Seconds
(without alignments)
9637.703 Million cell updates/sec

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Perfect score: 1713
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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 7338684 seqs, 3274456166 residues

Total number of hits satisfying chosen parameters: 14677368

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_NA:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1694.6	98.9	1712	9	US-09-981-353-189	Sequence 189, App
2	1694.6	98.9	1712	14	US-10-158-646-42	Sequence 42, Appl
3	1570.6	91.7	2844	14	US-10-198-846-13134	Sequence 13134, A
4	1452.4	84.8	2799	9	US-09-880-107-3756	Sequence 3756, Ap
5	1451.4	84.7	1991	14	US-10-057-834A-1	Sequence 1, Appli
6	1450	84.6	1855	9	US-09-880-107-2120	Sequence 2120, Ap
7	1450	84.6	1855	11	US-09-968-007A-368	Sequence 368, App
8	1450	84.6	1855	11	US-09-968-007A-735	Sequence 735, App
9	1450	84.6	1855	20	US-10-783-528-57	Sequence 57, Appl
10	1450	84.6	1855	21	US-10-843-641A-6838	Sequence 6838, Ap
11	1450	84.6	1855	21	US-10-843-641A-7205	Sequence 7205, Ap
12	1443.6	84.3	1854	14	US-10-205-522-39	Sequence 39, Appl
13	1436.4	83.9	1714	9	US-09-981-353-193	Sequence 193, App
14	1374	80.2	1639	18	US-10-468-125-18	Sequence 18, Appl
15	1354.2	79.1	2092	14	US-10-205-522-7	Sequence 7, Appli
16	1343	78.4	2093	9	US-09-880-107-3842	Sequence 3842, Ap
17	1190.8	69.5	1829	16	US-10-252-157-24	Sequence 24, Appl
18	1188.8	69.4	1976	14	US-10-205-522-112	Sequence 112, App
19	1188.8	69.4	2090	9	US-09-880-107-3292	Sequence 3292, Ap
20	1178	68.8	2150	9	US-09-981-353-45	Sequence 45, Appl
21	1178	68.8	2150	16	US-10-252-157-25	Sequence 25, Appl
22	1154.6	67.4	2123	9	US-09-880-107-3286	Sequence 3286, Ap
23	1128.8	65.9	1413	13	US-10-060-311-1	Sequence 1, Appli
24	1128.8	65.9	1413	19	US-10-778-300-1	Sequence 1, Appli
25	1128.8	65.9	1413	24	US-11-013-907-1	Sequence 1, Appli
26	1075.8	62.8	1614	18	US-10-381-898-24	Sequence 24, Appl
27	1014.2	59.2	1662	18	US-10-307-817-117	Sequence 117, App
28	997.8	58.2	1608	21	US-10-498-788-57	Sequence 57, Appl
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31	928.6	54.2	1606	17	US-10-042-865-27	Sequence 27, Appl
32	928.6	54.2	1606	18	US-10-072-012-151	Sequence 151, App
33	870.2	50.8	1844	14	US-10-175-523-59	Sequence 59, Appl
34	870.2	50.8	1844	24	US-11-099-266-59	Sequence 59, Appl
35	833	48.6	2634	17	US-10-388-934-169	Sequence 169, App
36	832.6	48.6	1947	18	US-10-152-319A-2121	Sequence 2121, Ap
37	832.6	48.6	1947	21	US-10-486-706-279	Sequence 279, App
38	828.6	48.4	1593	18	US-10-152-319A-1908	Sequence 1908, Ap
39	797	46.5	1224	18	US-10-381-898-32	Sequence 32, Appl
40	751.2	43.9	1756	15	US-10-235-994-27	Sequence 27, Appl
41	744.4	43.5	3006	9	US-09-962-678-1	Sequence 1, Appli
42	744.4	43.5	3006	17	US-10-184-648-38	Sequence 38, Appl
43	742.8	43.4	1636	9	US-09-981-353-165	Sequence 165, App
44	742.8	43.4	1636	17	US-10-258-080-11	Sequence 11, Appl
45	742.8	43.4	1705	18	US-10-114-270-51	Sequence 51, Appl

ALIGNMENTS

RESULT 1
US-09-981-353-189
; Sequence 189, Application US/09981353
; Patent No. US20020160382A1
; GENERAL INFORMATION:
; APPLICANT: Lasek, Amy W.
; APPLICANT: Jones, David A.
; TITLE OF INVENTION: GENES EXPRESSED IN COLON CANCER
; FILE REFERENCE: PA-0038 US
; CURRENT APPLICATION NUMBER: US/09/981,353
; CURRENT FILING DATE: 2001-10-11
; NUMBER OF SEQ ID NOS: 194
; SOFTWARE: PERL Program
; SEQ ID NO 189
; LENGTH: 1712
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No. US20020160382A1 480489.5
US-09-981-353-189

Query Match 98.9%; Score 1694.6; DB 9; Length 1712;
Best Local Similarity 99.7%; Pred. No. 0;
Matches 1703; Conservative 0; Mismatches 4; Indels 1; Gaps 1;

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; Sequence 42, Application US/10158646
; Publication No. US20030073105A1
; GENERAL INFORMATION:
; APPLICANT: Lasek, Amy K.W.
; APPLICANT: Sornasse, Thierry
; TITLE OF INVENTION: GENES EXPRESSED IN COLON CANCER
; FILE REFERENCE: PA-0030-1 US
; CURRENT APPLICATION NUMBER: US/10/158,646
; CURRENT FILING DATE: 2002-05-29
; PRIOR APPLICATION NUMBER: 60/295,239
; PRIOR FILING DATE: 2001-05-31
; NUMBER OF SEQ ID NOS: 78
; SOFTWARE: PERL Program
; SEQ ID NO 42
; LENGTH: 1712
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No. US20030073105A1 480489.3
US-10-158-646-42

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Best Local Similarity 99.7%; Pred. No. 0;
Matches 1708; Conservative 0; Mismatches 4; Indels 1; Gaps 1;

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Qy      1681 GATTGTTATGCAAGATTTCTTTCTTCCTGTGAC 1713

Db      1680 GATTGTTATGCAAGATTTCTTTCTTCCTGTGAC 1712
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RESULT 3
US-10-198-846-13134
; Sequence 13134, Application US/10198846
; Publication No. US20030099974A1
; GENERAL INFORMATION:
; APPLICANT: Lillie, James
; APPLICANT: Xu, Yongyao
; APPLICANT: Wang, Youzhen
; APPLICANT: Steinmann, Kathleen
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS
; TITLE OF INVENTION: FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
; TITLE OF INVENTION: THERAPY OF BREAST CANCER
; FILE REFERENCE: MRI-049
; CURRENT APPLICATION NUMBER: US/10/198,846
; CURRENT FILING DATE: 2002-07-18
; PRIOR APPLICATION NUMBER: 60/306,220
; PRIOR FILING DATE: 2001-07-18
; NUMBER OF SEQ ID NOS: 14084
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 13134
; LENGTH: 2844
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 2824, 2825, 2826, 2827, 2828, 2829, 2830, 2831, 2832, 2833,
; LOCATION: 2834, 2835, 2836, 2837, 2838, 2839, 2840, 2841, 2842, 2843,
; LOCATION: 2844
; OTHER INFORMATION: n = A,T,C or G
US-10-198-846-13134

Query Match 91.7%; Score 1570.6; DB 14; Length 2844;
Best Local Similarity 96.4%; Pred. No. 0;
Matches 1628; Conservative 0; Mismatches 59; Indels 2; Gaps 2;

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Qy          3 CGCATTGCACCAGGATGACTCTGAAATGGACTTCAGTTCTTCTGCTGATACATCTCCAGT 62
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Db         20 CGCATTGCACCAGGATGACTCTGAAATGGACTTCAGTTCTTCTGCTGATACATCT-CAGT 78

Qy         63 TGTTACTTTAGCTCTGGGAGTTGTGGAAAAGTGCTGGTGTGGGCCGCAGAATACAGCCAT 122
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         79 TGTTACTTTAGCTCTGGGAGTTGTGGAAAAGTGCTGGTGTGGGCCGCAGAATACAGCCAT 138

Qy        123 TGGATGAATATGAAGACAATCCTGAAAGAGCTTGTTCAGAGAGGTCATGAGGTGACTGTA 182
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        139 TGGATGAATATGAAGACAATCCTGAAAGAGCTTGTTCAGAGAGGTCATGAGGTGACTGTA 198

Qy        183 CTGGCATCTTCAGCTTCCATTCTTTTTGATCCCAATGATGCATCCACTCTTAAATTTGAA 242
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        199 CTGGCATCTTCAGCTTCCATTCTTTTTGATCCCAATGATGCATCCACTCTTAAATTTGAA 258

Qy        243 GTTTATCCTACATCTTTAACTAAAACTGAATTTGAGAATATCATCATGCAACAGGTTAAG 302
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        259 GTTTATCCTACATCTTTAACTAAAACTGAATTTGAGAATATCATCATGCAACAGGTTAAG 318

Qy        303 AGATGGTCAGACATTCGAAAAGATAGCTTTTGGTTATATTTTTCACAAGAACAAGAAATC 362
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        319 AGATGGTCAGACATTCGAAAAGATAGCTTTTGGTTATATTTTTCACAAGAACAAGAAATC 378

Qy        363 CTGTGGGAATTATATGACATATTTAGAAACTTCTGTAAAGATGTAGTTTCAAATAAGAAA 422
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        379 CTGTGGGAATTATATGACATATTTAGAAACTTCTGTAAAGATGTAGTTTCAAATAAGAAA 438

Qy        423 GTTATGAAAAAACTACAAGAGTCAAGATTTGACATCGTTTTTGCAGATGCTGTTTTTCCC 482
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        439 GTTATGAAAAAACTACAAGAGTCAAGATTTGACATCGTTTTTGCAGATGCTGTTTTTCCC 498

Qy        483 TGTGGTGAGCTGCTGGCTGCGCTACTTAACATACGGTTTGTGTACAGTCTCCGCTTTACT 542
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||| |||
Db        499 TGTGGTGAGCTGCTGGCTGCGCTACTTAACATACCGTTTGTGTACAGTCTCCGCTTCACT 558

Qy        543 CCTGGCTACACAATTGAAAGGCACAGTGGAGGACTGATTTTCCCTCCTTCCTACATACCT 602
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        559 CCTGGCTACACAATTGAAAGGCACAGTGGAGGACTGATTTTCCCTCCTTCCTACATACCT 618

Qy        603 ATTGTTATGTCAAAATTAAGTGATCAAATGACTTTCATGGAGAGGGTAAAAAATATGATC 662
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        619 ATTGTTATGTCAAAATTAAGTGATCAAATGACTTTCATGGAGAGGGTAAAAAATATGATC 678

Qy        663 TATGTGCTTTATTTTGACTTTTGGTTCCAAATGTCTGATATGAAGAAGTGGGATCAGTTT 722
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        679 TATGTGCTTTATTTTGACTTTTGGTTCCAAATGTCTGATATGAAGAAGTGGGATCAGTTT 738

Qy        723 TACAGTGAAGTTTTAGGAAGACCCACTACCTTATTTGAGACAATGGGAAAAGCTGACATA 782
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        739 TACAGTGAAGTTTTAGGAAGACCCACTACCTTATTTGAGACAATGGGAAAAGCTGACATA 798

Qy        783 TGGCTTATGCGAAACTCCTGGAGTTTTCAATTTCCTCATCCATTCTTACCAAACGTTGAT 842
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        799 TGGCTTATGCGAAACTCCTGGAGTTTTCAATTTCCTCATCCATTCTTACCAAACGTTGAT 858

Qy        843 TTTGTTGGAGGATTCCACTGGCAAACCTGCCAAACCCCTACCTAAGGAAATGGAGGAGTT 902
              |||||||||||||||||| ||||||||||||||||||||||||||||||||||||||||
Db        859 TTTGTTGGAGGATTCCACT-GCAAACCTGCCAAACCCCTACCTAAGGAAATGGAGGAGTT 917

Qy        903 TGTACAGAGCTCTGGAGAAAATGGTGTTGTGGTGTTTTCTCTGGGGTCAGTGATAAGTAA 962
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        918 TGTACAGAGCTCTGGAGAAAATGGTGTTGTGGTGTTTTCTCTGGGGTCAGTGATAAGTAA 977

Qy        963 CATGACAGCAGAAAGGGCCAATGTAATTGCAACAGCCCTTGCCAAGATCCCACAAAAGGT 1022
              |||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||
Db        978 CATGACAGCAGAAAGGGCCAACGTAATTGCAACAGCCCTTGCCAAGATCCCACAAAAGGT 1037

Qy       1023 TCTGTGGAGATTTGATGGGAATAAACCAGATGCCTTAGGTCTCAATACTCGGCTGTATAA 1082
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1038 TCTGTGGAGATTTGATGGGAATAAACCAGATGCCTTAGGTCTCAATACTCGGCTGTATAA 1097

Qy       1083 GTGGATACCCCAGAATGACCTTCTAGGTCATCCAAAAACCAGAGCTTTTATAACTCATGG 1142
              |||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||
Db       1098 GTGGATACCCCAGAATGACCTTCTAGGTCTTCCAAAAACCAGAGCTTTTATAACTCATGG 1157

Qy       1143 TGGAGCCAATGGCATCTATGAGGCAATCTACCATGGGATCCCTATGGTGGGCATTCCATT 1202
              |||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||
Db       1158 TGGAGCCAATGGCATCTATGAGGCAATCTACCATGGGATCCCTATGGTAGGCATTCCATT 1217

Qy       1203 GTTTTGGGATCAACCTGATAACATTGCTCACATGAAGGCCAAGGGAGCAGCTGTTAGATT 1262
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||| |
Db       1218 GTTTTGGGATCAACCTGATAACATTGCTCACATGAAGGCCAAGGGAGCAGCTGTTAGACT 1277

Qy       1263 GGACTTCAACACAATGTCGAGTACAGACCTGCTGAATGCACTGAAGACAGTAATTAATGA 1322
              ||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1278 GGACTTCCACACAATGTCGAGTACAGACCTGCTGAATGCACTGAAGACAGTAATTAATGA 1337

Qy       1323 TCCTTTATATAAAGAGAATATTATGAAATTATCAAGAATTCAACATGATCAACCAGTAAA 1382
              ||||| |||||||||||||||||||||||||||||||||||||||||||||||||| ||
Db       1338 TCCTTCATATAAAGAGAATATTATGAAATTATCAAGAATTCAACATGATCAACCAGTGAA 1397

Qy       1383 GCCCCTGGATCGAGCAGTCTTCTGGATTGAATTTGTCATGCCCCACAAAGGAGCCAAACA 1442
              |||||||||||||||||||||||||||||||||||||| ||||||||||||||||||
Db       1398 GCCCCTGGATCGAGCAGTCTTCTGGATTGAATTTGTCATGCGCCACAAAGGAGCCAAACA 1457

Qy       1443 CCTTCGAGTTGCAGCCCATGACCTCACCTGGTTCCAGTACCACTCTTTGGATGTGATTGG 1502
              |||||||||||||||||  ||||||||||||||||||||||||||||||||||||||||
Db       1458 TCTTCGAGTTGCAGCCCACAACCTCACCTGGTTCCAGTACCACTCTTTGGATGTGATTGG 1517

Qy       1503 GTTTCTGCTGGCCTGTGTGGCAACTGTGATATTTATCATCACAAAGTTTTGTCTGTTTTG 1562
              ||| |||||||| |||||||||||| ||| ||||||||||||||||| ||||||||||||
Db       1518 GTTCCTGCTGGCTTGTGTGGCAACCGTGCTATTTATCATCACAAAGTGTTGTCTGTTTTG 1577

Qy       1563 TTTCTGGAAGTTTGCTAGAAAAGGGAAGAAGGGAAAAAGAGATTAGTTATGTCTGACATT 1622
              |||||||||||||||||||||| |||||||||||||| |||||||||| ||||| |||
Db       1578 TTTCTGGAAGTTTGCTAGAAAAGGAAAGAAGGGAAAAAGGGATTAGTTATATCTGAGATT 1637

Qy       1623 TGAAGCTGGAAAACCAGATAGATAGGACAACTTCAGTTTATTCCAGCAAGAAAGAAAAGA 1682
              |||||||||  ||      |  || | | |       |     |  | ||||  |    ||
Db       1638 TGAAGCTGGGGAATTCCGTTTATTGAAGATTCAGGTTAACCTGAATCAAGTTAACCCAGT 1697

Qy       1683 TTGTTATGC 1691
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Db       1698 CTCAAATGC 1706
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RESULT 4
US-09-880-107-3756
; Sequence 3756, Application US/09880107
; Patent No. US20020142981A1
; GENERAL INFORMATION:
; APPLICANT: Horne, Darci T.
; APPLICANT: Vockley, Joseph G.
; APPLICANT: Scherf, Uwe
; APPLICANT: Gene Logic, Inc.
; TITLE OF INVENTION: Gene Expression Profiles in Liver Cancer
; FILE REFERENCE: 44921-5028-WO
; CURRENT APPLICATION NUMBER: US/09/880,107
; CURRENT FILING DATE: 2001-06-14
; PRIOR APPLICATION NUMBER: US 60/211,379
; PRIOR FILING DATE: 2000-06-14
; PRIOR APPLICATION NUMBER: US 60/237,054
; PRIOR FILING DATE: 2000-10-02
; NUMBER OF SEQ ID NOS: 3950
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3756
; LENGTH: 2799
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Genbank Accession No. US20020142981A1 X63359
US-09-880-107-3756

Query Match 84.8%; Score 1452.4; DB 9; Length 2799;

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Best Local Similarity   92.2%;  Pred. No. 0;
Matches 1553;  Conservative    0;  Mismatches  126;  Indels    5;  Gaps    2;

Qy          8 TGCACCAGGATGACTCTGAAATGGACTTCAGTTCTTCTGCTGATACATCTCCAGTTGTTA 67
              ||||| |||||| |||||||||||||| ||||||| ||| |   ||     ||||| |||
Db          2 TGCACAAGGATGGCTCTGAAATGGACTACAGTTCTGCTGATACAACT----CAGTTTTTA 57

Qy         68 CTTTAGCTCTGGGAGTTGTGGAAAAGTGCTGGTGTGGGCCGCAGAATACAGCCATTGGAT 127
              |||||||||||||||||||||||| |||||||| |||||||||||||||||| ||||||
Db         58 CTTTAGCTCTGGGAGTTGTGGAAAGGTGCTGGTATGGGCCGCAGAATACAGCCTTTGGAT 117

Qy        128 GAATATGAAGACAATCCTGAAAGAGCTTGTTCAGAGAGGTCATGAGGTGACTGTACTGGC 187
              ||||||||||||||||||||||||| |||||||||||||||||||||||||||||||||
Db        118 GAATATGAAGACAATCCTGAAAGAACTTGTTCAGAGAGGTCATGAGGTGACTGTACTGGC 177

Qy        188 ATCTTCAGCTTCCATTCTTTTTGATCCCAATGATGCATCCACTCTTAAATTTGAAGTTTA 247
              |||||||||||||||||||||||||||||| ||  |||||||||||||| ||||||||||
Db        178 ATCTTCAGCTTCCATTCTTTTTGATCCCAACGACTCATCCACTCTTAAACTTGAAGTTTA 237

Qy        248 TCCTACATCTTTAACTAAAACTGAATTTGAGAATATCATCATGCAACAGGTTAAGAGATG 307
              |||||||||||||||||||||||||||||||||||||||||||||  ||||||||||||
Db        238 TCCTACATCTTTAACTAAAACTGAATTTGAGAATATCATCATGCAATTGGTTAAGAGATT 297

Qy        308 GTCAGACATTCGAAAAGATAGCTTTTGGTTATATTTTTCACAAGAACAAGAAATCCTGTG 367
              ||||||  |||| ||||||||  |||||||| ||||||||||||||||||||||||||||
Db        298 GTCAGAAATTCAAAAAGATACATTTTGGTTACCTTTTTCACAAGAACAAGAAATCCTGTG 357

Qy        368 GGAATTATATGACATATTTAGAAACTTCTGTAAAGATGTAGTTTCAAATAAGAAAGTTAT 427
              || | |  |||||||| ||||||||||||||||||||||||||||||||||||| ||||
Db        358 GGCAATTAATGACATAATTAGAAACTTCTGTAAAGATGTAGTTTCAAATAAGAAACTTAT 417

Qy        428 GAAAAAACTACAAGAGTCAAGATTTGACATCGTTTTTGCAGATGCTGTTTTTCCCTGTGG 487
              |||||||||||||||||||||||||||||||||||||||||||||  ||| ||||||||
Db        418 GAAAAAACTACAAGAGTCAAGATTTGACATCGTTTTTGCAGATGCTTATTTACCCTGTGG 477

Qy        488 TGAGCTGCTGGCTGCGCTACTTAACATACGGTTTGTGTACAGTCTCCGCTTTACTCCTGG 547
              |||||||||||||| |||| |||||||||  |||||||||||| | |||| | ||||||
Db        478 TGAGCTGCTGGCTGAGCTATTTAACATACCCTTTGTGTACAGTCACAGCTTCAGTCCTGG 537

Qy        548 CTACACAATTGAAAGGCACAGTGGAGGACTGATTTTCCCTCCTTCCTACATACCTATTGT 607
              |||| || |||||||||||||||||||| | |||||||||||||||||| ||||| ||||
Db        538 CTACTCATTTGAAAGGCACAGTGGAGGATTTATTTTCCCTCCTTCCTACGTACCTGTTGT 597

Qy        608 TATGTCAAAATTAAGTGATCAAATGACTTTCATGGAGAGGGTAAAAAATATGATCTATGT 667
              |||||||||||||||||||||||||||||||||||||||||||||||||||| |||||||
Db        598 TATGTCAAAATTAAGTGATCAAATGACTTTCATGGAGAGGGTAAAAAATATGCTCTATGT 657

Qy        668 GCTTTATTTTGACTTTTGGTTCCAAATGTCTGATATGAAGAAGTGGGATCAGTTTTACAG 727
              |||||||||||||||||||||||||| | | ||||||||||||||||||||||||||||
Db        658 GCTTTATTTTGACTTTTGGTTCCAAATATTTAATATGAAGAAGTGGGATCAGTTTTACAG 717

Qy        728 TGAAGTTTTAGGAAGACCCACTACCTTATTTGAGACAATGGGAAAAGCTGACATATGGCT 787
              |||||||||||||||||||||||| |||| |||||||||| | ||||||||||||||||
Db        718 TGAAGTTTTAGGAAGACCCACTACATTATCTGAGACAATGAGGAAAGCTGACATATGGCT 777

Qy        788 TATGCGAAACTCCTGGAGTTTTCAATTTCCTCATCCATTCTTACCAAACGTTGATTTTGT 847
              |||||||||||||||| |||| |||||||||||||||||||||||||| ||||||||||
Db        778 TATGCGAAACTCCTGGAATTTTAAATTTCCTCATCCATTCTTACCAAATGTTGATTTTGT 837

Qy        848 TGGAGGATTCCACTGGCAAACCTGCCAAACCCCTACCTAAGGAAATGGAGGAGTTTGTAC 907
              ||||||| |||||| ||||||||||||||||||||||||||||||||||||||||||||
Db        838 TGGAGGACTCCACT-GCAAACCTGCCAAACCCCTACCTAAGGAAATGGAGGAGTTTGTAC 896

Qy        908 AGAGCTCTGGAGAAAATGGTGTTGTGGTGTTTTCTCTGGGGTCAGTGATAAGTAACATGA 967
              |||||||||||||||||||||||||||||||||||||||||||||| || | ||||||||||
Db        897 AGAGCTCTGGAGAAAATGGTGTTGTGGTGTTTTCTCTGGGGTCAATGGTCAGTAACATGA 956

Qy        968 CAGCAGAAAGGGCCAATGTAATTGCAACAGCCCTTGCCAAGATCCCACAAAAGGTTCTGT 1027
              ||| |||||||||||| |||||||||||||||||||||||||||||||||||||||| |
Db        957 CAGAAGAAAGGGCCAACGTAATTGCAACAGCCCTTGCCAAGATCCCACAAAAGGTTCTTT 1016

Qy       1028 GGAGATTTGATGGGAATAAACCAGATGCCTTAGGTCTCAATACTCGGCTGTATAAGTGGA 1087
              |||||||||||||||||||||||||||||||||||||||||||||| ||||| |||||||

Db       1017 GGAGATTTGATGGGAATAAACCAGATGCCTTAGGTCTCAATACTCGACTGTACAAGTGGA 1076

Qy       1088 TACCCCAGAATGACCTTCTAGGTCATCCAAAAACCAGAGCTTTTATAACTCATGGTGGAG 1147
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1077 TACCCCAGAATGACCTTCTAGGTCATCCAAAAACCAGAGCTTTTATAACTCATGGTGGAG 1136

Qy       1148 CCAATGGCATCTATGAGGCAATCTACCATGGGATCCCTATGGTGGGCATTCCATTGTTTT 1207
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1137 CCAATGGCATCTATGAGGCAATCTACCATGGGATCCCTATGGTGGGCATTCCATTGTTTT 1196

Qy       1208 GGGATCAACCTGATAACATTGCTCACATGAAGGCCAAGGGAGCAGCTGTTAGATTGGACT 1267
                |||||||||||||| ||||||||||||||||||||||||||||||||||| ||||||
Db       1197 TTGATCAACCTGATAATATTGCTCACATGAAGGCCAAGGGAGCAGCTGTTAGAGTGGACT 1256

Qy       1268 TCAACACAATGTCGAGTACAGACCTGCTGAATGCACTGAAGACAGTAATTAATGATCCTT 1327
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1257 TCAACACAATGTCGAGTACAGACCTGCTGAATGCACTGAAGACAGTAATTAATGATCCTT 1316

Qy       1328 TATATAAAGAGAATATTATGAAATTATCAAGAATTCAACATGATCAACCAGTAAAGCCCC 1387
              |||||||||||||||||||||||||||||||||||||||||||||||||||| |||||||
Db       1317 CATATAAAGAGAATATTATGAAATTATCAAGAATTCAACATGATCAACCAGTGAAGCCCC 1376

Qy       1388 TGGATCGAGCAGTCTTCTGGATTGAATTTGTCATGCCCCACAAAGGAGCCAAACACCTTC 1447
              |||||||||||||||||||||||||||||||||||||||||||||||||||| ||||||
Db       1377 TGGATCGAGCAGTCTTCTGGATTGAATTTGTCATGCGCCACAAAGGAGCCAAACATCTTC 1436

Qy       1448 GAGTTGCAGCCCATGACCTCACCTGGTTCCAGTACCACTCTTTGGATGTGATTGGGTTTC 1507
              |||||||||||||  ||||||||||||||||||||||||||||||||||||||||||| |
Db       1437 GAGTTGCAGCCCACAACCTCACCTGGTTCCAGTACCACTCTTTGGATGTGATTGGGTTCC 1496

Qy       1508 TGCTGGCCTGTGTGGCAACTGTGATATTTATCATCACAAAGTTTTGTCTGTTTTGTTTCT 1567
              ||||||| ||||||||||||| ||| ||||||||||||||||||| ||||||||||||||
Db       1497 TGCTGGCTTGTGTGGCAACCGTGCTATTTATCATCACAAAGTGTTGTCTGTTTTGTTTCT 1556

Qy       1568 GGAAGTTTGCTAGAAAAGGGAAGAAGGGAAAAAGAGATTAGTTATGTCTGACATTTGAAG 1627
              |||||||||||||||||| |||||||||||||| |||||||||| |||| |||||||||
Db       1557 GGAAGTTTGCTAGAAAAGGAAAGAAGGGAAAAAGGGATTAGTTATATCTGAGATTTGAAG 1616

Qy       1628 CTGGAAAACCAGATAGATAGGACAACTTCAGTTTATTCCAGCAAGAAAGAAAAGATTGTT 1687
              ||||  ||     |  || | | |     |  | ||||  |   ||  |
Db       1617 CTGGGGAATTCCGTTTATTGAAGATTCAGGTTAACCTGAATCAAGTTAACCCAGTCTCAA 1676

Qy       1688 ATGC 1691
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Db       1677 ATGC 1680
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RESULT 5
US-10-057-834A-1
; Sequence 1, Application US/10057834A
; Publication No. US20030099960A1
; GENERAL INFORMATION:
;  APPLICANT: RATAIN, MARK J.
;  APPLICANT:  INNOCENTI, FEDERICO
;  APPLICANT:  DAS, SOMA
;  APPLICANT:  IYER, LALITHA
;  APPLICANT:  SAWYER, MICHAEL
;  TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR OPTIMIZING UGT2B7 SUBSTRATE DOSINGS
;  TITLE OF INVENTION:  PREDICTING UGT2B7 SUBSTRATE TOXICITY
;  FILE REFERENCE: ARCD:358US
;  CURRENT APPLICATION NUMBER: US/10/057,834A
;  CURRENT FILING DATE:  2002-08-22
;  PRIOR APPLICATION NUMBER: UNKNOWN
;  PRIOR FILING DATE: 2002-01-25
;  NUMBER OF SEQ ID NOS: 78
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
;   LENGTH: 1991
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (151)..(1740)
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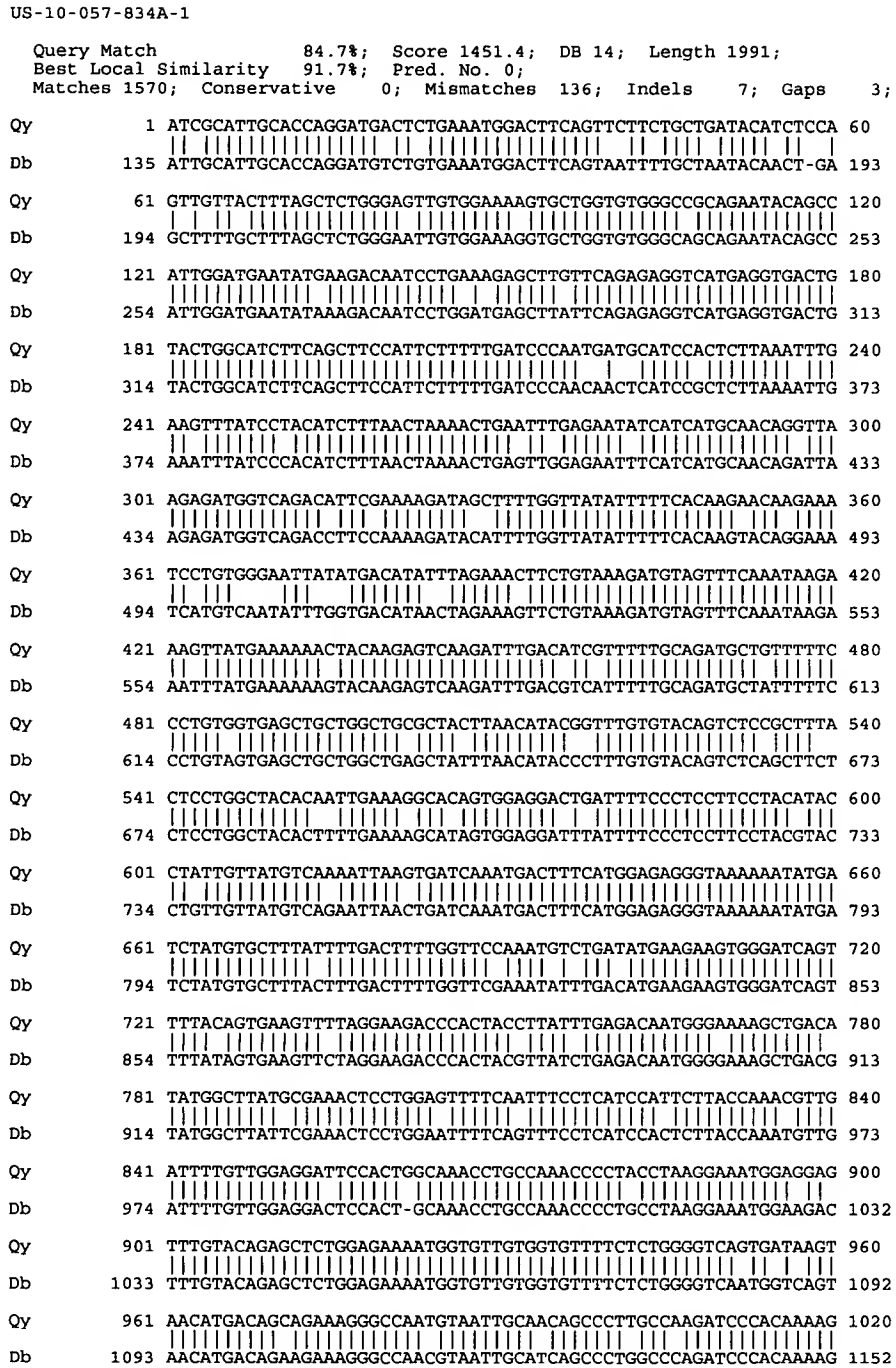
US-10-057-834A-1

Query Match 84.7%; Score 1451.4; DB 14; Length 1991;
Best Local Similarity 91.7%; Pred. No. 0;
Matches 1570; Conservative 0; Mismatches 136; Indels 7; Gaps 3;



RESULT 6
US-09-880-107-2120
; Sequence 2120, Application US/09880107
; Patent No. US20020142981A1
; GENERAL INFORMATION:
; APPLICANT: Horne, Darci T.
; APPLICANT: Vockley, Joseph G.
; APPLICANT: Scherf, Uwe
; APPLICANT: Gene Logic, Inc.
; TITLE OF INVENTION: Gene Expression Profiles in Liver Cancer
; FILE REFERENCE: 44921-5028-WO
; CURRENT APPLICATION NUMBER: US/09/880,107
; CURRENT FILING DATE: 2001-06-14
; PRIOR APPLICATION NUMBER: US 60/211,379
; PRIOR FILING DATE: 2000-06-14
; PRIOR APPLICATION NUMBER: US 60/237,054
; PRIOR FILING DATE: 2000-10-02
; NUMBER OF SEQ ID NOS: 3950
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2120
; LENGTH: 1855
; TYPE: DNA
; ORGANISM: Homo sapiens

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;   FEATURE:
;   OTHER INFORMATION: Genbank Accession No. US20020142981A1 J05428
US-09-880-107-2120

  Query Match             84.6%;  Score 1450;  DB 9;  Length 1855;
  Best Local Similarity   91.7%;  Pred. No. 0;
  Matches 1568;  Conservative    0;  Mismatches  135;  Indels    7;  Gaps    3;

Qy          4 GCATTGCACCAGGATGACTCTGAAATGGACTTCAGTTCTTCTGCTGATACATCTCCAGTT 63
              ||||||||||||||| || ||||||||||||||  || |||| ||||| ||  || |
Db          2 GCATTGCACCAGGATGTCTGTGAAATGGACTTCAGTAATTTTGCTAATACAACTG-AGCT 60

Qy         64 GTTACTTTAGCTCTGGGAGTTGTGGAAAAGTGCTGGTGTGGGCCGCAGAATACAGCCATT 123
               || ||||||||||||| |||||||| |||||||||||||| ||||||||||||||||||
Db         61 TTTGCTTTAGCTCTGGGAATTGTGGAAAGGTGCTGGTGTGGGCAGCAGAATACAGCCATT 120

Qy        124 GGATGAATATGAAGACAATCCTGAAAGAGCTTGTTCAGAGAGGTCATGAGGTGACTGTAC 183
              |||||||||| |||||||||||  | ||||| ||||||||||||||||||||||||||||
Db        121 GGATGAATATAAAGACAATCCTGGATGAGCTTATTCAGAGAGGTCATGAGGTGACTGTAC 180

Qy        184 TGGCATCTTCAGCTTCCATTCTTTTTGATCCCAATGATGCATCCACTCTTAAAATTTGAAG 243
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Db        181 TGGCATCTTCAGCTTCCATTCTTTTTGATCCCAACAACTCATCCGCTCTTAAAATTGAAA 240

Qy        244 TTTATCCTACATCTTTAACTAAAACTGAATTTGAGAATATCATCATGCAACAGGTTAAGA 303
              |||||||||||||||||||||||| || |||||| ||||||||||||| ||||||
Db        241 TTTATCCCACATCTTTAACTAAAACTGAGTTGGAGAATTTCATCATGCAACAGATTAAGA 300

Qy        304 GATGGTCAGACATTCGAAAAGATAGCTTTTGGTTATATTTTTCACAAGAACAAGAAATCC 363
              |||||||||| ||| ||||||||  |||||||||||||||||||||| ||| ||||||
Db        301 GATGGTCAGACCTTCCAAAAGATACATTTTGGTTATATTTTTCACAAGTACAGGAAATCA 360

Qy        364 TGTGGGAATTATATGACATATTTAGAAACTTCTGTAAAGATGTAGTTTCAAATAAGAAAG 423
              |||   |||   |||||||  |||||| ||||||||||||||||||||||||||||||
Db        361 TGTCAATATTTGGTGACATAACTAGAAAGTTCTGTAAAGATGTAGTTTCAAATAAGAAAT 420

Qy        424 TTATGAAAAAACTACAAGAGTCAAGATTTGACATCGTTTTTGCAGATGCTGTTTTTCCCT 483
              |||||||||| |||||||||||||||||| || |||||||||||| |||||||||
Db        421 TTATGAAAAAAGTACAAGAGTCAAGATTTGACGTCATTTTTGCAGATGCTATTTTTCCCT 480

Qy        484 GTGGTGAGCTGCTGGCTGCGCTACTTAACATACGGTTTGTGTACAGTCTCCGCTTTACTC 543
              || |||||||||||||| |||| |||||||||  ||||||||||||||| |||| |||
Db        481 GTAGTGAGCTGCTGGCTGAGCTATTTAACATACCCTTTGTGTACAGTCTCAGCTTCTCTC 540

Qy        544 CTGGCTACACAATTGAAAGGCACAGTGGAGGACTGATTTTCCCTCCTTCCTACATACCTA 603
              ||||||||||  |||||| ||| ||||||||| | ||||||||||||||||| |||||
Db        541 CTGGCTACACTTTTGAAAAGCATAGTGGAGGATTTATTTTCCCTCCTTCCTACGTACCTG 600

Qy        604 TTGTTATGTCAAAATTAAGTGATCAAATGACTTTCATGGAGAGGGTAAAAAATATGATCT 663
              |||||||||||| |||||| |||||||||||||||||||||||||||||||||||||||
Db        601 TTGTTATGTCAGAATTAACTGATCAAATGACTTTCATGGAGAGGGTAAAAAATATGATCT 660

Qy        664 ATGTGCTTTATTTTGACTTTTGGTTCCAAATGTCTGATATGAAGAAGTGGGATCAGTTTT 723
              |||||||||| |||||||||||||| |||| | ||| ||||||||||||||||||||||
Db        661 ATGTGCTTTACTTTGACTTTTGGTTCGAAATATTTGACATGAAGAAGTGGGATCAGTTTT 720

Qy        724 ACAGTGAAGTTTTAGGAAGACCCACTACCTTATTTGAGACAATGGGAAAAGCTGACATAT 783
              | |||||||||| |||||||||||||||| |||| |||||||||||| |||||||||| |||
Db        721 ATAGTGAAGTTCTAGGAAGACCCACTACGTTATCTGAGACAATGGGGAAAGCTGACGTAT 780

Qy        784 GGCTTATGCGAAACTCCTGGAGTTTTCAATTTCCTCATCCATTCTTACCAAACGTTGATT 843
              |||||||  |||||||||||||| |||||| |||||||||||| ||||||||| |||||||
Db        781 GGCTTATTCGAAACTCCTGGAATTTTCAGTTTCCTCATCCACTCTTACCAAATGTTGATT 840

Qy        844 TTGTTGGAGGATTCCACTGGCAAACCTGCCAAACCCCTACCTAAGGAAATGGAGGAGTTT 903
              |||||||||| |||||| |||||||||||||||||| |||||||||||||| || |||
Db        841 TTGTTGGAGGACTCCACT-GCAAACCTGCCAAACCCCTGCCTAAGGAAATGGAAGACTTT 899

Qy        904 GTACAGAGCTCTGGAGAAAATGGTGTTGTGGTGTTTTCTCTGGGGTCAGTGATAAGTAAC 963
              |||||||||||||||||||||||||||||||||||||||||||||||| || | ||||||
Db        900 GTACAGAGCTCTGGAGAAAATGGTGTTGTGGTGTTTTCTCTGGGGTCAATGGTCAGTAAC 959

Qy        964 ATGACAGCAGAAAGGGCCAATGTAATTGCAACAGCCCTTGCCAAGATCCCACAAAAGGTT 1023
              ||||||| |||||||||||| |||||||| ||||||| ||| ||||||||||||||||||
Db        960 ATGACAGAAGAAAGGGCCAACGTAATTGCATCAGCCCTGGCCCAGATCCCACAAAAGGTT 1019

Qy       1024 CTGTGGAGATTTGATGGGAATAAACCAGATGCCTTAGGTCTCAATACTCGGCTGTATAAG 1083
              ||||||||||||||||||||||||||||||||||| |||||||||||||||||||||||
Db       1020 CTGTGGAGATTTGATGGGAATAAACCAGATACCTTAGGTCTCAATACTCGGCTGTATAAG 1079

Qy       1084 TGGATACCCCAGAATGACCTTCTAGGTCATCCAAAAACCAGAGCTTTTATAACTCATGGT 1143
              |||||||||||||||||||||||||||||||||||||||| |||||||||||||||||||
Db       1080 TGGATACCCCAGAATGACCTTCTAGGTCATCCAAAGACCAGAGCTTTTATAACTCATGGT 1139

Qy       1144 GGAGCCAATGGCATCTATGAGGCAATCTACCATGGGATCCCTATGGTGGGCATTCCATTG 1203
              |||||||||||||||| |||||||||||||||||||||||||||||| |||||||||
Db       1140 GGAGCCAATGGCATCTACGAGGCAATCTACCATGGGATCCCTATGGTGGGGATTCCATTG 1199

Qy       1204 TTTTGGGATCAACCTGATAACATTGCTCACATGAAGGCCAAGGGAGCAGCTGTTAGATTG 1263
              |||   |||||||||||||||||||||||||||||||||||||||| ||||||||||||| ||
Db       1200 TTTGCCGATCAACCTGATAACATTGCTCACATGAAGGCCAGGGGAGCAGCTGTTAGAGTG 1259

Qy       1264 GACTTCAACACAATGTCGAGTACAGACCTGCTGAATGCACTGAAGACAGTAATTAATGAT 1323
              |||||||||||||||||||||||||| |||||||||| |||||| ||||||||||||
Db       1260 GACTTCAACACAATGTCGAGTACAGACTTGCTGAATGCATTGAAGAGAGTAATTAATGAT 1319

Qy       1324 CCTTTATATAAAGAGAATATTATGAAATTATCAAGAATTCAACATGATCAACCAGTAAAG 1383
              |||| |||||||||||| |||||||||||||||||||||||||||||||||||| |||
Db       1320 CCTTCATATAAAGAGAATGTTATGAAATTATCAAGAATTCAACATGATCAACCAGTGAAG 1379

Qy       1384 CCCCTGGATCGAGCAGTCTTCTGGATTGAATTTGTCATGCCCCACAAAGGAGCCAAACAC 1443
              |||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||
Db       1380 CCCCTGGATCGAGCAGTCTTCTGGATTGAATTTGTCATGCGCCACAAAGGAGCTAAACAC 1439

Qy       1444 CTTCGAGTTGCAGCCCATGACCTCACCTGGTTCCAGTACCACTCTTTGGATGTGATTGGG 1503
              ||||| |||||||||||| ||||||||||||||||||||||||||||||||||||||||
Db       1440 CTTCGGGTTGCAGCCCACGACCTCACCTGGTTCCAGTACCACTCTTTGGATGTGATTGGG 1499

Qy       1504 TTTCTGCTGGCCTGTGTGGCAACTGTGATATTTATCATCACAAAGTTTTGTCTGTTTTGT 1563
              || ||||||| |||||||||||||||||||||||| ||||||| | ||||||||||||
Db       1500 TTCCTGCTGGTCTGTGTGGCAACTGTGATATTTATCGTCACAAAATGTTGTCTGTTTTGT 1559

Qy       1564 TTCTGGAAGTTTGCTAGAAAAGGGAAGAAGGGAAAAAGAGATTAGTTATGTCTGACATTT 1623
              |||||||||||||||||||||||| |||||||||||||  |||||||||| |||| ||||
Db       1560 TTCTGGAAGTTTGCTAGAAAAGCAAAGAAGGGAAAAAATGATTAGTTATATCTGAGATTT 1619

Qy       1624 GAAGCTGGAAAACCAGATAGATAGGACAACTTCAGTTTATTCCAGCAAGAAAGAAAAGAT 1683
              |||||||||||||| ||||| |  ||| |||||||||||||||||||||     ||||||
Db       1620 GAAGCTGGAAAACCTGATAGGTGAGACTACTTCAGTTTATTCCAGCAAG-----AAAGAT 1674

Qy       1684 TGTTATGCAAGATTTCTTTCTTCCTGTGAC 1713
              ||| |||||||||||||||||||||| |||
Db       1675 TGTGATGCAAGATTTCTTTCTTCCTGAGAC 1704


RESULT 7
US-09-968-007A-368
; Sequence 368, Application US/09968007A
; Publication No. US20040115625A1
; GENERAL INFORMATION:
;  APPLICANT: Ebner, Reinhard
;  TITLE OF INVENTION: Cancer Gene Determination and Therapeutic Screening Usining Signa
;  TITLE OF INVENTION:  Gene Sets
;  FILE REFERENCE: 689290-71
;  CURRENT APPLICATION NUMBER: US/09/968,007A
;  CURRENT FILING DATE:  2001-10-02
;  PRIOR APPLICATION NUMBER: US/60/237,172
;  PRIOR FILING DATE: 2000-10-02
;  PRIOR APPLICATION NUMBER: US/60/237,173
;  PRIOR FILING DATE: 2000-10-02
;  PRIOR APPLICATION NUMBER: US/60/237,278
;  PRIOR FILING DATE: 2000-10-02
;  PRIOR APPLICATION NUMBER: US/60/237,294
;  PRIOR FILING DATE: 2000-10-02
;  PRIOR APPLICATION NUMBER: US/60/237,295
;  PRIOR FILING DATE: 2000-10-02
```

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;  PRIOR APPLICATION NUMBER: US/60/237,316
;  PRIOR FILING DATE: 2000-10-02
;  NUMBER OF SEQ ID NOS: 1001
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 368
;   LENGTH: 1855
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-968-007A-368

  Query Match             84.6%;  Score 1450;  DB 11;  Length 1855;
  Best Local Similarity   91.7%;  Pred. No. 0;
  Matches 1568;  Conservative    0;  Mismatches  135;  Indels    7;  Gaps    3;

Qy          4 GCATTGCACCAGGATGACTCTGAAATGGACTTCAGTTCTTCTGCTGATACATCTCCAGTT 63
              |||||||||||||||| || ||||||||||||||||   || |||| ||||| ||  || |
Db          2 GCATTGCACCAGGATGTCTGTGAAATGGACTTCAGTAATTTTGCTAATACAACTG-AGCT 60

Qy         64 GTTACTTTAGCTCTGGGAGTTGTGGAAAAGTGCTGGTGTGGGCCGCAGAATACAGCCATT 123
               || |||||||||||||| ||||||||| |||||||||||||| ||||||||||||||||
Db         61 TTTGCTTTAGCTCTGGGAATTGTGGAAAGGTGCTGGTGTGGGCAGCAGAATACAGCCATT 120

Qy        124 GGATGAATATGAAGACAATCCTGAAAGAGCTTGTTCAGAGAGGTCATGAGGTGACTGTAC 183
              |||||||||| |||||||||||| | |||||| ||||||||||||||||||||||||||
Db        121 GGATGAATATAAAGACAATCCTGGATGAGCTTATTCAGAGAGGTCATGAGGTGACTGTAC 180

Qy        184 TGGCATCTTCAGCTTCCATTCTTTTTGATCCCAATGATGCATCCACTCTTAAAATTTGAAG 243
              ||||||||||||||||||||||||||||||||   |  ||||| |||||||| |||||
Db        181 TGGCATCTTCAGCTTCCATTCTTTTTGATCCCAACAACTCATCCGCTCTTAAAATTGAAA 240

Qy        244 TTTATCCTACATCTTTAACTAAAACTGAATTTGAGAATATCATCATGCAACAGGTTAAGA 303
              ||||||| |||||||||||||||||| || |||||| |||||||||||||| ||||||
Db        241 TTTATCCCACATCTTTAACTAAAACTGAGTTGGAGAATTTCATCATGCAACAGATTAAGA 300

Qy        304 GATGGTCAGACATTCGAAAAGATAGCTTTTGGTTATATTTTTCACAAGAACAAGAAATCC 363
              |||||||||| ||| |||||||| |||||||||||||||||||||||| ||| ||||||
Db        301 GATGGTCAGACCTTCCAAAAGATACATTTTGGTTATATTTTTCACAAGTACAGGAAATCA 360

Qy        364 TGTGGGAATTATATGACATATTTAGAAACTTCTGTAAAGATGTAGTTTCAAATAAGAAAG 423
              |||    |||   ||||||| |||||| |||||||||||||||||||||||||||||
Db        361 TGTCAATATTTGGTGACATAACTAGAAAGTTCTGTAAAGATGTAGTTTCAAATAAGAAAT 420

Qy        424 TTATGAAAAAACTACAAGAGTCAAGATTTGACATCGTTTTTGCAGATGCTGTTTTTCCCT 483
              |||||||||| |||||||||||||||||| || |||||||||||||| |||||||||
Db        421 TTATGAAAAAAGTACAAGAGTCAAGATTTGACGTCATTTTTGCAGATGCTATTTTTCCCT 480

Qy        484 GTGGTGAGCTGCTGGCTGCGCTACTTAACATACGGTTTGTGTACAGTCTCCGCTTTACTC 543
              || |||||||||||||| |||| |||||||||  ||||||||||||||| ||||  |||
Db        481 GTAGTGAGCTGCTGGCTGAGCTATTTAACATACCCTTTGTGTACAGTCTCAGCTTCTCTC 540

Qy        544 CTGGCTACACAATTGAAAGGCACAGTGGAGGACTGATTTTCCCTCCTTCCTACATACCTA 603
              |||||||||  |||||| ||| ||||||||| | |||||||||||||||||| |||||
Db        541 CTGGCTACACTTTTGAAAAGCATAGTGGAGGATTTATTTTCCCTCCTTCCTACGTACCTG 600

Qy        604 TTGTTATGTCAAAATTAAGTGATCAAATGACTTTCATGGAGAGGGTAAAAAATATGATCT 663
              |||||||||| |||||| ||||||||||||||||||||||||||||||||||||||||
Db        601 TTGTTATGTCAGAATTAACTGATCAAATGACTTTCATGGAGAGGGTAAAAAATATGATCT 660

Qy        664 ATGTGCTTTATTTTGACTTTTGGTTCCAAATGTCTGATATGAAGAAGTGGGATCAGTTTT 723
              |||||||||| |||||||||||||||| |||| | ||| ||||||||||||||||||||
Db        661 ATGTGCTTTACTTTGACTTTTGGTTCGAAATATTTGACATGAAGAAGTGGGATCAGTTTT 720

Qy        724 ACAGTGAAGTTTTAGGAAGACCCACTACCTTATTTGAGACAATGGGAAAAGCTGACATAT 783
              | |||||||||| |||||||||||||||| |||| |||||||||||| |||||||| |||
Db        721 ATAGTGAAGTTCTAGGAAGACCCACTACGTTATCTGAGACAATGGGGAAAGCTGACGTAT 780

Qy        784 GGCTTATGCGAAACTCCTGGAGTTTTCAATTTCCTCATCCATTCTTACCAAACGTTGATT 843
              ||||||| |||||||||||||| |||||| |||||||||||  |||||||||| |||||||
Db        781 GGCTTATTCGAAACTCCTGGAATTTTCAGTTTCCTCATCCACTCTTACCAAATGTTGATT 840

Qy        844 TTGTTGGAGGATTCCACTGGCAAACCTGCCAAACCCCTACCTAAGGAAATGGAGGAGTTT 903
              |||||||||| |||||| |||||||||||||||||| |||||||||||||| || |||
Db        841 TTGTTGGAGGACTCCACT-GCAAACCTGCCAAACCCCTGCCTAAGGAAATGGAAGACTTT 899

Qy        904 GTACAGAGCTCTGGAGAAAATGGTGTTGTGGTGTTTTCTCTGGGGTCAGTGATAAGTAAC 963
              |||||||||||||||||||||||||||||||||||||||||||||||| || | ||||||
Db        900 GTACAGAGCTCTGGAGAAAATGGTGTTGTGGTGTTTTCTCTGGGGTCAATGGTCAGTAAC 959

Qy        964 ATGACAGCAGAAAGGGCCAATGTAATTGCAACAGCCCTTGCCAAGATCCCACAAAAGGTT 1023
              ||||||| |||||||||||| ||||||||| ||||||| ||| ||||||||||||||||||
Db        960 ATGACAGAAGAAAGGGCCAACGTAATTGCATCAGCCCTGGCCCAGATCCCACAAAAGGTT 1019

Qy       1024 CTGTGGAGATTTGATGGGAATAAACCAGATGCCTTAGGTCTCAATACTCGGCTGTATAAG 1083
              |||||||||||||||||||||||||||||||| ||||||||||||||||||||||||||
Db       1020 CTGTGGAGATTTGATGGGAATAAACCAGATACCTTAGGTCTCAATACTCGGCTGTATAAG 1079

Qy       1084 TGGATACCCCAGAATGACCTTCTAGGTCATCCAAAAACCAGAGCTTTTATAACTCATGGT 1143
              |||||||||||||||||||||||||||||||||||||||| ||||||||||||||||||||
Db       1080 TGGATACCCCAGAATGACCTTCTAGGTCATCCAAAGACCAGAGCTTTTATAACTCATGGT 1139

Qy       1144 GGAGCCAATGGCATCTATGAGGCAATCTACCATGGGATCCCTATGGTGGGCATTCCATTG 1203
              |||||||||||||||| |||||||||||||||||||||||||||||| |||||||||
Db       1140 GGAGCCAATGGCATCTACGAGGCAATCTACCATGGGATCCCTATGGTGGGGATTCCATTG 1199

Qy       1204 TTTTGGGATCAACCTGATAACATTGCTCACATGAAGGCCAAGGGAGCAGCTGTTAGATTG 1263
              |||   |||||||||||||||||||||||||||||||| |||||||||||||||| ||
Db       1200 TTTGCCGATCAACCTGATAACATTGCTCACATGAAGGCCAGGGGAGCAGCTGTTAGAGTG 1259

Qy       1264 GACTTCAACACAATGTCGAGTACAGACCTGCTGAATGCACTGAAGACAGTAATTAATGAT 1323
              |||||||||||||||||||||||||||||||| |||||| ||||||||||||
Db       1260 GACTTCAACACAATGTCGAGTACAGACTTGCTGAATGCATTGAAGAGAGTAATTAATGAT 1319

Qy       1324 CCTTTATATAAAGAGAATATTATGAAATTATCAAGAATTCAACATGATCAACCAGTAAAG 1383
              |||| |||||||||||| ||||||||||||||||||||||||||||||||||| |||
Db       1320 CCTTCATATAAAGAGAATGTTATGAAATTATCAAGAATTCAACATGATCAACCAGTGAAG 1379

Qy       1384 CCCCTGGATCGAGCAGTCTTCTGGATTGAATTTGTCATGCCCCACAAAGGAGCCAAACAC 1443
              |||||||||||||||||||||||||||||||||||||||| |||||||||||| ||||||
Db       1380 CCCCTGGATCGAGCAGTCTTCTGGATTGAATTTGTCATGCGCCACAAAGGAGCTAAACAC 1439

Qy       1444 CTTCGAGTTGCAGCCCATGACCTCACCTGGTTCCAGTACCACTCTTTGGATGTGATTGGG 1503
              ||||| |||||||||||| ||||||||||||||||||||||||||||||||||||||||
Db       1440 CTTCGGGTTGCAGCCCACGACCTCACCTGGTTCCAGTACCACTCTTTGGATGTGATTGGG 1499

Qy       1504 TTTCTGCTGGCCTGTGTGGCAACTGTGATATTTATCATCACAAAGTTTTGTCTGTTTTGT 1563
              || ||||||| |||||||||||||||||||||||| ||||||| | ||||||||||||
Db       1500 TTCCTGCTGGTCTGTGTGGCAACTGTGATATTTATCGTCACAAAATGTTGTCTGTTTTGT 1559

Qy       1564 TTCTGGAAGTTTGCTAGAAAAGGGAAGAAGGGAAAAAGAGATTAGTTATGTCTGACATTT 1623
              |||||||||||||||||||  |||||||||||| |||||||| |||| ||||
Db       1560 TTCTGGAAGTTTGCTAGAAAAGCAAAGAAGGGAAAAAATGATTAGTTATATCTGAGATTT 1619

Qy       1624 GAAGCTGGAAAACCAGATAGATAGGACAACTTCAGTTTATTCCAGCAAGAAAGAAAAGAT 1683
              |||||||||||||| ||||| |  ||| |||||||||||||||||||     ||||||
Db       1620 GAAGCTGGAAAACCTGATAGGTGAGACTACTTCAGTTTATTCCAGCAAG-----AAAGAT 1674

Qy       1684 TGTTATGCAAGATTTCTTTCTTCCTGTGAC 1713
              ||| |||||||||||||||||||| |||
Db       1675 TGTGATGCAAGATTTCTTTCTTCCTGAGAC 1704


RESULT 8
US-09-968-007A-735
; Sequence 735, Application US/09968007A
; Publication No. US20040115625A1
; GENERAL INFORMATION:
;  APPLICANT: Ebner, Reinhard
;  TITLE OF INVENTION: Cancer Gene Determination and Therapeutic Screening Usining Signa
;  TITLE OF INVENTION:  Gene Sets
;  FILE REFERENCE: 689290-71
;  CURRENT APPLICATION NUMBER: US/09/968,007A
;  CURRENT FILING DATE:  2001-10-02
;  PRIOR APPLICATION NUMBER: US/60/237,172
;  PRIOR FILING DATE: 2000-10-02
;  PRIOR APPLICATION NUMBER: US/60/237,173
;  PRIOR FILING DATE: 2000-10-02
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;  PRIOR APPLICATION NUMBER: US/60/237,278
;  PRIOR FILING DATE: 2000-10-02
;  PRIOR APPLICATION NUMBER: US/60/237,294
;  PRIOR FILING DATE: 2000-10-02
;  PRIOR APPLICATION NUMBER: US/60/237,295
;  PRIOR FILING DATE: 2000-10-02
;  PRIOR APPLICATION NUMBER: US/60/237,316
;  PRIOR FILING DATE: 2000-10-02
;  NUMBER OF SEQ ID NOS: 1001
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 735
;   LENGTH: 1855
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-968-007A-735

  Query Match            84.6%;  Score 1450;  DB 11;  Length 1855;
  Best Local Similarity  91.7%;  Pred. No. 0;
  Matches 1568;  Conservative    0;  Mismatches  135;  Indels    7;  Gaps    3;

Qy          4 GCATTGCACCAGGATGACTCTGAAATGGACTTCAGTTCTTCTGCTGATACATCTCCAGTT 63
Db          2 GCATTGCACCAGGATGTCTGTGAAATGGACTTCAGTAATTTTGCTAATACAACTG-AGCT 60

Qy         64 GTTACTTTAGCTCTGGGAGTTGTGGAAAAGTGCTGGTGTGGGCCGCAGAATACAGCCATT 123
Db         61 TTTGCTTTAGCTCTGGGAATTGTGGAAAGGTGCTGGTGTGGGCAGCAGAATACAGCCATT 120

Qy        124 GGATGAATATGAAGACAATCCTGAAAGAGCTTGTTCAGAGAGGTCATGAGGTGACTGTAC 183
Db        121 GGATGAATATAAAGACAATCCTGGATGAGCTTATTCAGAGAGGTCATGAGGTGACTGTAC 180

Qy        184 TGGCATCTTCAGCTTCCATTCTTTTTGATCCCAATGATGCATCCACTCTTAAATTTGAAG 243
Db        181 TGGCATCTTCAGCTTCCATTCTTTTTGATCCCAACAACTCATCCGCTCTTAAAATTGAAA 240

Qy        244 TTTATCCTACATCTTTAACTAAAACTGAATTTGAGAATATCATCATGCAACAGGTTAAGA 303
Db        241 TTTATCCCACATCTTTAACTAAAACTGAGTTGGAGAATTTCATCATGCAACAGATTAAGA 300

Qy        304 GATGGTCAGACATTCGAAAAGATAGCTTTTGGTTATATTTTTCACAAGAACAAGAAATCC 363
Db        301 GATGGTCAGACCTTCCAAAAGATACATTTTGGTTATATTTTTCACAAGTACAGGAAATCA 360

Qy        364 TGTGGGAATTATATGACATATTTAGAAACTTCTGTAAAGATGTAGTTTCAAATAAGAAAG 423
Db        361 TGTCAATATTTGGTGACATAACTAGAAAGTTCTGTAAAGATGTAGTTTCAAATAAGAAAT 420

Qy        424 TTATGAAAAAACTACAAGAGTCAAGATTTGACATCGTTTTTGCAGATGCTGTTTTTCCCT 483
Db        421 TTATGAAAAAAGTACAAGAGTCAAGATTTGACGTCATTTTTGCAGATGCTATTTTTCCCT 480

Qy        484 GTGGTGAGCTGCTGGCTGCGCTACTTAACATACGGTTTGTGTACAGTCTCCGCTTTACTC 543
Db        481 GTAGTGAGCTGCTGGCTGAGCTATTTAACATACCCTTTGTGTACAGTCTCAGCTTCTCTC 540

Qy        544 CTGGCTACACAATTGAAAGGCACAGTGGAGGACTGATTTCCCTCCTTCCTACATACCTA 603
Db        541 CTGGCTACACTTTTGAAAAGCATAGTGGAGGATTTATTTCCCTCCTTCCTACGTACCTG 600

Qy        604 TTGTTATGTCAAAATTAAGTGATCAAATGACTTTCATGGAGAGGGTAAAAAATATGATCT 663
Db        601 TTGTTATGTCAGAATTAACTGATCAAATGACTTTCATGGAGAGGGTAAAAAATATGATCT 660

Qy        664 ATGTGCTTTATTTTGACTTTTGGTTCCAAATGTCTGATATGAAGAAGTGGGATCAGTTTT 723
Db        661 ATGTGCTTTACTTTGACTTTTGGTTCGAAATATTTGACATGAAGAAGTGGGATCAGTTTT 720

Qy        724 ACAGTGAAGTTTTAGGAAGACCCACTACCTTATTTGAGACAATGGGAAAAGCTGACATAT 783
Db        721 ATAGTGAAGTTCTAGGAAGACCCACTACGTTATCTGAGACAATGGGGAAAGCTGACGTAT 780

Qy        784 GGCTTATGCGAAACTCCTGGAGTTTTCAATTTCCTCATCCATTCTTACCAAACGTTGATT 843
Db        781 GGCTTATTCGAAACTCCTGGAATTTTCAGTTTCCTCATCCACTCTTACCAAATGTTGATT 840

Qy        844 TTGTTGGAGGATTCCACTGGCAAACCTGCCAAACCCCTACCTAAGGAAATGGAGGAGTTT 903
Db        841 TTGTTGGAGGACTCCACT-GCAAACCTGCCAAACCCCTGCCTAAGGAAATGGAAGACTTT 899

Qy        904 GTACAGAGCTCTGGAGAAAATGGTGTTGTGGTGTTTTCTCTGGGGTCAGTGATAAGTAAC 963
Db        900 GTACAGAGCTCTGGAGAAAATGGTGTTGTGGTGTTTTCTCTGGGGTCAATGGTCAGTAAC 959

Qy        964 ATGACAGCAGAAAGGGCCAATGTAATTGCAACAGCCCTTGCCAAGATCCCACAAAAGGTT 1023
Db        960 ATGACAGAAGAAAGGGCCAACGTAATTGCATCAGCCCTGGCCCAGATCCCACAAAAGGTT 1019

Qy       1024 CTGTGGAGATTTGATGGGAATAAACCAGATGCCTTAGGTCTCAATACTCGGCTGTATAAG 1083
Db       1020 CTGTGGAGATTTGATGGGAATAAACCAGATACCTTAGGTCTCAATACTCGGCTGTATAAG 1079

Qy       1084 TGGATACCCCAGAATGACCTTCTAGGTCATCCAAAAACCAGAGCTTTTATAACTCATGGT 1143
Db       1080 TGGATACCCCAGAATGACCTTCTAGGTCATCCAAAGACCAGAGCTTTTATAACTCATGGT 1139

Qy       1144 GGAGCCAATGGCATCTATGAGGCAATCTACCATGGGATCCCTATGGTGGGCATTCCATTG 1203
Db       1140 GGAGCCAATGGCATCTACGAGGCAATCTACCATGGGATCCCTATGGTGGGGATTCCATTG 1199

Qy       1204 TTTTGGGATCAACCTGATAACATTGCTCACATGAAGGCCAAGGGAGCAGCTGTTAGATTG 1263
Db       1200 TTTGCCGATCAACCTGATAACATTGCTCACATGAAGGCCAGGGGAGCAGCTGTTAGAGTG 1259

Qy       1264 GACTTCAACACAATGTCGAGTACAGACCTGCTGAATGCACTGAAGACAGTAATTAATGAT 1323
Db       1260 GACTTCAACACAATGTCGAGTACAGACTTGCTGAATGCATTGAAGAGAGTAATTAATGAT 1319

Qy       1324 CCTTTATATAAAGAGAATATTATGAAATTATCAAGAATTCAACATGATCAACCAGTAAAG 1383
Db       1320 CCTTCATATAAAGAGAATGTTATGAAATTATCAAGAATTCAACATGATCAACCAGTGAAG 1379

Qy       1384 CCCCTGGATCGAGCAGTCTTCTGGATTGAATTTGTCATGCCCCACAAAGGAGCCAAACAC 1443
Db       1380 CCCCTGGATCGAGCAGTCTTCTGGATTGAATTTGTCATGCGCCACAAAGGAGCTAAACAC 1439

Qy       1444 CTTCGAGTTGCAGCCCATGACCTCACCTGGTTCCAGTACCACTCTTTGGATGTGATTGGG 1503
Db       1440 CTTCGGGTTGCAGCCCACGACCTCACCTGGTTCCAGTACCACTCTTTGGATGTGATTGGG 1499

Qy       1504 TTTCTGCTGGCCTGTGTGGCAACTGTGATATTTATCATCACAAAGTTTTGTCTGTTTTGT 1563
Db       1500 TTCCTGCTGGTCTGTGTGGCAACTGTGATATTTATCGTCACAAAATGTTGTCTGTTTTGT 1559

Qy       1564 TTCTGGAAGTTTGCTAGAAAAGGGAAGAAGGGAAAAAGAGATTAGTTATGTCTGACATTT 1623
Db       1560 TTCTGGAAGTTTGCTAGAAAAGCAAAGAAGGGAAAAAATGATTAGTTATATCTGAGATTT 1619

Qy       1624 GAAGCTGGAAAACCAGATAGATAGGACAACTTCAGTTTATTCCAGCAAGAAAGAAAAGAT 1683
Db       1620 GAAGCTGGAAAACCTGATAGGTGAGACTACTTCAGTTTATTCCAGCAAG-----AAAGAT 1674

Qy       1684 TGTTATGCAAGATTTCTTTCTTCCTGTGAC 1713
Db       1675 TGTGATGCAAGATTTCTTTCTTCCTGAGAC 1704

RESULT 9
US-10-783-528-57
; Sequence 57, Application US/10783528
; Publication No. US20040219579A1
; GENERAL INFORMATION:
;  APPLICANT: Aziz, Natasha
;  APPLICANT:  Gish, Kurt
;  APPLICANT:  Wilson, Keith
;  APPLICANT:  Zlotnik, Albert
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;  TITLE OF INVENTION: METHODS OF DIAGNOSIS OF CANCER, COMPOSITIONS AND
;  FILE REFERENCE: 05882.0191.NPUS01
;  CURRENT APPLICATION NUMBER: US/10/783,528
;  CURRENT FILING DATE:  2004-02-19
;  NUMBER OF SEQ ID NOS: 116
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 57
;   LENGTH: 1855
;   TYPE: DNA
;   ORGANISM: Homo Sapiens
US-10-783-528-57

  Query Match             84.6%;  Score 1450;  DB 20;  Length 1855;
  Best Local Similarity   91.7%;  Pred. No. 0;
  Matches 1568;  Conservative    0;  Mismatches  135;  Indels    7;  Gaps    3;

Qy          4 GCATTGCACCAGGATGACTCTGAAATGGACTTCAGTTCTTCTGCTGATACATCTCCAGTT 63
              ||||||||||||||| || ||||||||||||||  || |||| ||||| ||  || |
Db          2 GCATTGCACCAGGATGTCTGTGAAATGGACTTCAGTAATTTTGCTAATACAACTG-AGCT 60

Qy         64 GTTACTTTAGCTCTGGGAGTTGTGGAAAAGTGCTGGTGTGGGCCGCAGAATACAGCCATT 123
               || |||||||||||||| ||||||||| |||||||||||||| ||||||||||||||||
Db         61 TTTGCTTTAGCTCTGGGAATTGTGGAAAGGTGCTGGTGTGGGCAGCAGAATACAGCCATT 120

Qy        124 GGATGAATATGAAGACAATCCTGAAAGAGCTTGTTCAGAGAGGTCATGAGGTGACTGTAC 183
              ||||||||| |||||||||| | |||||| ||||||||||||||||||||||||||||
Db        121 GGATGAATATAAAGACAATCCTGGATGAGCTTATTCAGAGAGGTCATGAGGTGACTGTAC 180

Qy        184 TGGCATCTTCAGCTTCCATTCTTTTTGATCCCAATGATGCATCCACTCTTAAATTTGAAG 243
              |||||||||||||||||||||||||||||||||  |  ||||| ||||||| |||||
Db        181 TGGCATCTTCAGCTTCCATTCTTTTTGATCCCAACAACTCATCCGCTCTTAAAATTGAAA 240

Qy        244 TTTATCCTACATCTTTAACTAAAACTGAATTTGAGAATATCATCATGCAACAGGTTAAGA 303
              ||||||| |||||||||||||||||||| || |||||| |||||||||||||| ||||||
Db        241 TTTATCCCACATCTTTAACTAAAACTGAGTTGGAGAATTTCATCATGCAACAGATTAAGA 300

Qy        304 GATGGTCAGACATTCGAAAAGATAGCTTTTGGTTATATTTTTCACAAGAACAAGAAATCC 363
              |||||||||| ||| |||||||  |||||||||||||||||||||| ||| ||||||
Db        301 GATGGTCAGACCTTCCAAAAGATACATTTTGGTTATATTTTTCACAAGTACAGGAAATCA 360

Qy        364 TGTGGGAATTATATGACATATTTAGAAACTTCTGTAAAGATGTAGTTTCAAATAAGAAAG 423
              |||    |||   |||||||  |||||| ||||||||||||||||||||||||||||||
Db        361 TGTCAATATTTGGTGACATAACTAGAAAGTTCTGTAAAGATGTAGTTTCAAATAAGAAAT 420

Qy        424 TTATGAAAAAACTACAAGAGTCAAGATTTGACATCGTTTTTGCAGATGCTGTTTTTCCCT 483
              |||||||||||| |||||||||||||||||||| || |||||||||||||| |||||||||
Db        421 TTATGAAAAAAGTACAAGAGTCAAGATTTGACGTCATTTTTGCAGATGCTATTTTTCCCT 480

Qy        484 GTGGTGAGCTGCTGGCTGCGCTACTTAACATACGGTTTGTGTACAGTCTCCGCTTTACTC 543
              || |||||||||||||| |||| ||||||||| |||||||||||||||| ||||  |||
Db        481 GTAGTGAGCTGCTGGCTGAGCTATTTAACATACCCTTTGTGTACAGTCTCAGCTTCTCTC 540

Qy        544 CTGGCTACACAATTGAAAGGCACAGTGGAGGACTGATTTTCCCTCCTTCCTACATACCTA 603
              ||||||||||  |||||| ||| |||||||||| | |||||||||||||||| ||||||
Db        541 CTGGCTACACTTTTGAAAAGCATAGTGGAGGATTTATTTTCCCTCCTTCCTACGTACCTG 600

Qy        604 TTGTTATGTCAAAATTAAGTGATCAAATGACTTTCATGGAGAGGGTAAAAAATATGATCT 663
              |||||||||||  |||||| ||||||||||||||||||||||||||||||||||||||||
Db        601 TTGTTATGTCAGAATTAACTGATCAAATGACTTTCATGGAGAGGGTAAAAAATATGATCT 660

Qy        664 ATGTGCTTTATTTTGACTTTTGGTTCCAAATGTCTGATATGAAGAAGTGGGATCAGTTTT 723
              |||||||||  |||||||||||||| |||| | ||| ||||||||||||||||||||||
Db        661 ATGTGCTTTACTTTGACTTTTGGTTCGAAATATTTGACATGAAGAAGTGGGATCAGTTTT 720

Qy        724 ACAGTGAAGTTTTAGGAAGACCCACTACCTTATTTGAGACAATGGGAAAAGCTGACATAT 783
              | |||||||||  |||||||||||||||| |||| |||||||||||  |||||||||| |||
Db        721 ATAGTGAAGTTCTAGGAAGACCCACTACGTTATCTGAGACAATGGGGAAAGCTGACGTAT 780

Qy        784 GGCTTATGCGAAACTCCTGGAGTTTTCAATTTCCTCATCCATTCTTACCAAACGTTGATT 843
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Db        781 GGCTTATTCGAAACTCCTGGAATTTTCAGTTTCCTCATCCACTCTTACCAAATGTTGATT 840

Qy        844 TTGTTGGAGGATTCCACTGGCAAACCTGCCAAACCCCTACCTAAGGAAATGGAGGAGTTT 903
              |||||||||||  |||||| |||||||||||||||||||||||  |||||||||||||| ||| |||
Db        841 TTGTTGGAGGACTCCACT-GCAAACCTGCCAAACCCCTGCCTAAGGAAATGGAAGACTTT 899

Qy        904 GTACAGAGCTCTGGAGAAAATGGTGTTGTGGTGTTTTCTCTGGGGTCAGTGATAAGTAAC 963
              |||||||||||||||||||||||||||||||||||||||||||||||||| || | ||||||
Db        900 GTACAGAGCTCTGGAGAAAATGGTGTTGTGGTGTTTTCTCTGGGGTCAATGGTCAGTAAC 959

Qy        964 ATGACAGCAGAAAGGGCCAATGTAATTGCAACAGCCCTTGCCAAGATCCCACAAAAGGTT 1023
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Db        960 ATGACAGAAGAAAGGGCCAACGTAATTGCATCAGCCCTGGCCCAGATCCCACAAAAGGTT 1019

Qy       1024 CTGTGGAGATTTGATGGGAATAAACCAGATGCCTTAGGTCTCAATACTCGGCTGTATAAG 1083
              |||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||||
Db       1020 CTGTGGAGATTTGATGGGAATAAACCAGATACCTTAGGTCTCAATACTCGGCTGTATAAG 1079

Qy       1084 TGGATACCCCAGAATGACCTTCTAGGTCATCCAAAAACCAGAGCTTTTATAACTCATGGT 1143
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Db       1080 TGGATACCCCAGAATGACCTTCTAGGTCATCCAAAGACCAGAGCTTTTATAACTCATGGT 1139

Qy       1144 GGAGCCAATGGCATCTATGAGGCAATCTACCATGGGATCCCTATGGTGGGCATTCCATTG 1203
              |||||||||||||||| ||||||||||||||||||||||||||||||||| |||||||||
Db       1140 GGAGCCAATGGCATCTACGAGGCAATCTACCATGGGATCCCTATGGTGGGGATTCCATTG 1199

Qy       1204 TTTTGGGATCAACCTGATAACATTGCTCACATGAAGGCCAAGGGAGCAGCTGTTAGATTG 1263
              |||   |||||||||||||||||||||||||||||||||| |||||||||||||||| ||
Db       1200 TTTGCCGATCAACCTGATAACATTGCTCACATGAAGGCCAGGGGAGCAGCTGTTAGAGTG 1259

Qy       1264 GACTTCAACACAATGTCGAGTACAGACCTGCTGAATGCACTGAAGACAGTAATTAATGAT 1323
              |||||||||||||||||||||||||||| |||||||||| |||||| ||||||||||||
Db       1260 GACTTCAACACAATGTCGAGTACAGACTTGCTGAATGCATTGAAGAGAGTAATTAATGAT 1319

Qy       1324 CCTTTATATAAAGAGAATATTATGAAATTATCAAGAATTCAACATGATCAACCAGTAAAG 1383
              |||| |||||||||||||| ||||||||||||||||||||||||||||||||||||| |||
Db       1320 CCTTCATATAAAGAGAATGTTATGAAATTATCAAGAATTCAACATGATCAACCAGTGAAG 1379

Qy       1384 CCCCTGGATCGAGCAGTCTTCTGGATTGAATTTGTCATGCCCCACAAAGGAGCCAAACAC 1443
              |||||||||||||||||||||||||||||||||||||||||| |||||||||||| ||||||
Db       1380 CCCCTGGATCGAGCAGTCTTCTGGATTGAATTTGTCATGCGCCACAAAGGAGCTAAACAC 1439

Qy       1444 CTTCGAGTTGCAGCCCATGACCTCACCTGGTTCCAGTACCACTCTTTGGATGTGATTGGG 1503
              ||||| |||||||||||| ||||||||||||||||||||||||||||||||||||||||||
Db       1440 CTTCGGGTTGCAGCCCACGACCTCACCTGGTTCCAGTACCACTCTTTGGATGTGATTGGG 1499

Qy       1504 TTTCTGCTGGCCTGTGTGGCAACTGTGATATTTATCATCACAAAGTTTTGTCTGTTTTGT 1563
              || |||||||  |||||||||||||||||||||||||||||||||| ||||||| |||||||
Db       1500 TTCCTGCTGGTCTGTGTGGCAACTGTGATATTTATCGTCACAAAATGTTGTCTGTTTTGT 1559

Qy       1564 TTCTGGAAGTTTGCTAGAAAAGGGAAGAAGGGAAAAAGAGATTAGTTATGTCTGACATTT 1623
              |||||||||||||||||||  ||||||||||||  |||||||||| ||||| ||||
Db       1560 TTCTGGAAGTTTGCTAGAAAAGCAAAGAAGGGAAAAAATGATTAGTTATATCTGAGATTT 1619

Qy       1624 GAAGCTGGAAAACCAGATAGATAGGACAACTTCAGTTTATTCCAGCAAGAAAGAAAAGAT 1683
              |||||||||||||| ||||| |  ||| ||||||||||||||||||||  ||||||
Db       1620 GAAGCTGGAAAACCTGATAGGTGAGACTACTTCAGTTTATTCCAGCAAG-----AAAGAT 1674

Qy       1684 TGTTATGCAAGATTTCTTTCTTCCTGTGAC 1713
              ||| |||||||||||||||||||||| |||
Db       1675 TGTGATGCAAGATTTCTTTCTTCCTGAGAC 1704


RESULT 10
US-10-843-641A-6838
; Sequence 6838, Application US/10843641A
; Publication No. US20050064454A1
; GENERAL INFORMATION:
;  APPLICANT: Avalon Pharmaceuticals, Inc.
;  TITLE OF INVENTION: Cancer Gene Determination and Therapeutic Screening Using
;  TITLE OF INVENTION:  Signature Gene Sets
;  FILE REFERENCE: 689290-189
;  CURRENT APPLICATION NUMBER: US/10/843,641A
;  CURRENT FILING DATE:  2004-05-12
;  PRIOR APPLICATION NUMBER: US/09/873,367
;  PRIOR FILING DATE: 2001-06-05
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;  PRIOR APPLICATION NUMBER: US/09/954,531
;  PRIOR FILING DATE: 2001-09-18
;  PRIOR APPLICATION NUMBER: US/09/954,456
;  PRIOR FILING DATE: 2001-09-25
;  PRIOR APPLICATION NUMBER: US/09/962,436
;  PRIOR FILING DATE: 2001-09-25
;  PRIOR APPLICATION NUMBER: US/09/962,832
;  PRIOR FILING DATE: 2001-09-25
;  PRIOR APPLICATION NUMBER: US/09/964,824
;  PRIOR FILING DATE: 2001-09-27
;  PRIOR APPLICATION NUMBER: US/09/967,768
;  PRIOR FILING DATE: 2001-09-28
;  PRIOR APPLICATION NUMBER: US/09/968,007
;  PRIOR FILING DATE: 2001-10-02
;  PRIOR APPLICATION NUMBER: US/09/969,347
;  PRIOR FILING DATE: 2001-10-02
;  PRIOR APPLICATION NUMBER: US/09/969,708
;  PRIOR FILING DATE: 2001-10-03
;  Remaining Prior Application data removed - See File Wrapper or PALM.
;  NUMBER OF SEQ ID NOS: 8447
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 6838
;   LENGTH: 1855
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)..(1855)
;   OTHER INFORMATION: n=a,t,g or c
US-10-843-641A-6838

  Query Match             84.6%;  Score 1450;  DB 21;  Length 1855;
  Best Local Similarity   91.7%;  Pred. No. 0;
  Matches 1568;  Conservative    0;  Mismatches  135;  Indels    7;  Gaps    3;

Qy          4 GCATTGCACCAGGATGACTCTGAAATGGACTTCAGTTCTTCTGCTGATACATCTCCAGTT 63
              |||||||||||||||| || ||||||||||||||||  || |||| ||||| ||  || |
Db          2 GCATTGCACCAGGATGTCTGTGAAATGGACTTCAGTAATTTTGCTAATACAACTG-AGCT 60

Qy         64 GTTACTTTAGCTCTGGGAGTTGTGGAAAAGTGCTGGTGTGGGCCGCAGAATACAGCCATT 123
               || |||||||||||||| ||||||||| |||||||||||||| ||||||||||||||||
Db         61 TTTGCTTTAGCTCTGGGAATTGTGGAAAGGTGCTGGTGTGGGCAGCAGAATACAGCCATT 120

Qy        124 GGATGAATATGAAGACAATCCTGAAAGAGCTTGTTCAGAGAGGTCATGAGGTGACTGTAC 183
              |||||||||| |||||||||| | |||||| ||||||||||||||||||||||||||||||
Db        121 GGATGAATATAAAGACAATCCTGGATGAGCTTATTCAGAGAGGTCATGAGGTGACTGTAC 180

Qy        184 TGGCATCTTCAGCTTCCATTCTTTTTGATCCCAATGATGCATCCACTCTTAAAATTTGAAG 243
              |||||||||||||||||||||||||||||||  |  ||||| |||||||| |||||
Db        181 TGGCATCTTCAGCTTCCATTCTTTTTGATCCCAACAACTCATCCGCTCTTAAAATTGAAA 240

Qy        244 TTTATCCTACATCTTTAACTAAAACTGAATTTGAGAATATCATCATGCAACAGGTTAAGA 303
              ||||||| |||||||||||||||||||| || |||||| |||||||||||||| ||||||
Db        241 TTTATCCCACATCTTTAACTAAAACTGAGTTGGAGAATTTCATCATGCAACAGATTAAGA 300

Qy        304 GATGGTCAGACATTCGAAAAGATAGCTTTTGGTTATATTTTTCACAAGAACAAGAAATCC 363
              |||||||||| ||| |||||||| |||||||||||||||||||||| ||| ||||||
Db        301 GATGGTCAGACCTTCCAAAAGATACATTTTGGTTATATTTTTCACAAGTACAGGAAATCA 360

Qy        364 TGTGGGAATTATATGACATATTTAGAAACTTCTGTAAAGATGTAGTTTCAAATAAGAAAG 423
              |||    |||   ||||||| |||||| ||||||||||||||||||||||||||||||
Db        361 TGTCAATATTTGGTGACATAACTAGAAAGTTCTGTAAAGATGTAGTTTCAAATAAGAAAT 420

Qy        424 TTATGAAAAAACTACAAGAGTCAAGATTTGACATCGTTTTTGCAGATGCTGTTTTTCCCT 483
              |||||||||| |||||||||||||||||||| || |||||||||||||| ||||||||||
Db        421 TTATGAAAAAAGTACAAGAGTCAAGATTTGACGTCATTTTTGCAGATGCTATTTTTCCCT 480

Qy        484 GTGGTGAGCTGCTGGCTGCGCTACTTAACATACGGTTTGTGTACAGTCTCCGCTTTACTC 543
              || |||||||||||||||| |||| |||||||||  |||||||||||||||| ||||  |||
Db        481 GTAGTGAGCTGCTGGCTGAGCTATTTAACATACCCTTTGTGTACAGTCTCAGCTTCTCTC 540

Qy        544 CTGGCTACACAATTGAAAGGCACAGTGGAGGACTGATTTTCCCTCCTTCCTACATACCTA 603
              ||||||||||  |||||| ||| ||||||||| | |||||||||||||||||| |||||  .

Db        541 CTGGCTACACTTTTGAAAAGCATAGTGGAGGATTTATTTTCCCTCCTTCCTACGTACCTG 600

Qy        604 TTGTTATGTCAAAATTAAGTGATCAAATGACTTTCATGGAGAGGGTAAAAAATATGATCT 663
              |||||||||| |||||| ||||||||||||||||||||||||||||||||||||||||
Db        601 TTGTTATGTCAGAATTAACTGATCAAATGACTTTCATGGAGAGGGTAAAAAATATGATCT 660

Qy        664 ATGTGCTTTATTTTGACTTTTGGTTCCAAATGTCTGATATGAAGAAGTGGGATCAGTTTT 723
              |||||||||| |||||||||||||| |||| | ||| ||||||||||||||||||||||
Db        661 ATGTGCTTTACTTTGACTTTTGGTTCGAAATATTTGACATGAAGAAGTGGGATCAGTTTT 720

Qy        724 ACAGTGAAGTTTTAGGAAGACCCACTACCTTATTTGAGACAATGGGAAAAGCTGACATAT 783
              | ||||||||| |||||||||||||| |||| |||||||||||| ||||||||| |||
Db        721 ATAGTGAAGTTCTAGGAAGACCCACTACGTTATCTGAGACAATGGGGAAAGCTGACGTAT 780

Qy        784 GGCTTATGCGAAACTCCTGGAGTTTTCAATTTCCTCATCCATTCTTACCAAACGTTGATT 843
              ||||||| |||||||||||| |||||| |||||||||||| |||||||||| |||||||
Db        781 GGCTTATTCGAAACTCCTGGAATTTTCAGTTTCCTCATCCACTCTTACCAAATGTTGATT 840

Qy        844 TTGTTGGAGGATTCCACTGGCAAACCTGCCAAACCCCTACCTAAGGAAATGGAGGAGTTT 903
              |||||||||| |||||| |||||||||||||||||||| |||||||||||||| || |||
Db        841 TTGTTGGAGGACTCCACT-GCAAACCTGCCAAACCCCTGCCTAAGGAAATGGAAGACTTT 899

Qy        904 GTACAGAGCTCTGGAGAAAATGGTGTTGTGGTGTTTTCTCTGGGGTCAGTGATAAGTAAC 963
              |||||||||||||||||||||||||||||||||||||||||||||||| || | ||||||
Db        900 GTACAGAGCTCTGGAGAAAATGGTGTTGTGGTGTTTTCTCTGGGGTCAATGGTCAGTAAC 959

Qy        964 ATGACAGCAGAAAGGGCCAATGTAATTGCAACAGCCCTTGCCAAGATCCCACAAAAGGTT 1023
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Db        960 ATGACAGAAGAAAGGGCCAACGTAATTGCATCAGCCCTGGCCCAGATCCCACAAAAGGTT 1019

Qy       1024 CTGTGGAGATTTGATGGGAATAAACCAGATGCCTTAGGTCTCAATACTCGGCTGTATAAG 1083
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Db       1020 CTGTGGAGATTTGATGGGAATAAACCAGATACCTTAGGTCTCAATACTCGGCTGTATAAG 1079

Qy       1084 TGGATACCCCAGAATGACCTTCTAGGTCATCCAAAAACCAGAGCTTTTATAACTCATGGT 1143
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Db       1080 TGGATACCCCAGAATGACCTTCTAGGTCATCCAAAGACCAGAGCTTTTATAACTCATGGT 1139

Qy       1144 GGAGCCAATGGCATCTATGAGGCAATCTACCATGGGATCCCTATGGTGGGCATTCCATTG 1203
              |||||||||||||||| ||||||||||||||||||||||||||||||| |||||||||
Db       1140 GGAGCCAATGGCATCTACGAGGCAATCTACCATGGGATCCCTATGGTGGGGATTCCATTG 1199

Qy       1204 TTTTGGGATCAACCTGATAACATTGCTCACATGAAGGCCAAGGGAGCAGCTGTTAGATTG 1263
              |||   |||||||||||||||||||||||||||||||||||||||||||||||||| ||
Db       1200 TTTGCCGATCAACCTGATAACATTGCTCACATGAAGGCCAGGGGAGCAGCTGTTAGAGTG 1259

Qy       1264 GACTTCAACACAATGTCGAGTACAGACCTGCTGAATGCACTGAAGACAGTAATTAATGAT 1323
              |||||||||||||||||||||||||||||| |||||||||| |||||| ||||||||||||
Db       1260 GACTTCAACACAATGTCGAGTACAGACTTGCTGAATGCATTGAAGAGAGTAATTAATGAT 1319

Qy       1324 CCTTTATATAAAGAGAATATTATGAAATTATCAAGAATTCAACATGATCAACCAGTAAAG 1383
              |||| |||||||||||| |||||||||||||||||||||||||||||||||||||| |||
Db       1320 CCTTCATATAAAGAGAATGTTATGAAATTATCAAGAATTCAACATGATCAACCAGTGAAG 1379

Qy       1384 CCCCTGGATCGAGCAGTCTTCTGGATTGAATTTGTCATGCCCCACAAAGGAGCCAAACAC 1443
              |||||||||||||||||||||||||||||||||||||||||||||| |||||||||| ||||||
Db       1380 CCCCTGGATCGAGCAGTCTTCTGGATTGAATTTGTCATGCGCCACAAAGGAGCTAAACAC 1439

Qy       1444 CTTCGAGTTGCAGCCCATGACCTCACCTGGTTCCAGTACCACTCTTTGGATGTGATTGGG 1503
              ||||| |||||||||| |||||||||||||||||||||||||||||||||||||||||||
Db       1440 CTTCGGGTTGCAGCCCACGACCTCACCTGGTTCCAGTACCACTCTTTGGATGTGATTGGG 1499

Qy       1504 TTTCTGCTGGCCTGTGTGGCAACTGTGATATTTATCATCACAAAGTTTTGTCTGTTTTGT 1563
              || ||||||| |||||||||||||||||||||||| ||||||| | ||||||||||||||
Db       1500 TTCCTGCTGGTCTGTGTGGCAACTGTGATATTTATCGTCACAAAATGTTGTCTGTTTTGT 1559

Qy       1564 TTCTGGAAGTTTGCTAGAAAAGGGAAGAAGGGAAAAAGAGATTAGTTATGTCTGACATTT 1623
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Db       1560 TTCTGGAAGTTTGCTAGAAAAGCAAAGAAGGGAAAAAATGATTAGTTATATCTGAGATTT 1619

Qy       1624 GAAGCTGGAAAACCAGATAGATAGGACAACTTCAGTTTATTCCAGCAAGAAAGAAAAGAT 1683
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Db       1620 GAAGCTGGAAAACCTGATAGGTGAGACTACTTCAGTTTATTCCAGCAAG-----AAAGAT 1674
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Qy       1684 TGTTATGCAAGATTTCTTTCTTCCTGTGAC 1713
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Db       1675 TGTGATGCAAGATTTCTTTCTTCCTGAGAC 1704


RESULT 11
US-10-843-641A-7205
; Sequence 7205, Application US/10843641A
; Publication No. US20050064454A1
; GENERAL INFORMATION:
;  APPLICANT: Avalon Pharmaceuticals, Inc.
;  TITLE OF INVENTION: Cancer Gene Determination and Therapeutic Screening Using
;  TITLE OF INVENTION:  Signature Gene Sets
;  FILE REFERENCE: 689290-189
;  CURRENT APPLICATION NUMBER: US/10/843,641A
;  CURRENT FILING DATE:  2004-05-12
;  PRIOR APPLICATION NUMBER: US/09/873,367
;  PRIOR FILING DATE: 2001-06-05
;  PRIOR APPLICATION NUMBER: US/09/954,531
;  PRIOR FILING DATE: 2001-09-18
;  PRIOR APPLICATION NUMBER: US/09/954,456
;  PRIOR FILING DATE: 2001-09-25
;  PRIOR APPLICATION NUMBER: US/09/962,436
;  PRIOR FILING DATE: 2001-09-25
;  PRIOR APPLICATION NUMBER: US/09/962,832
;  PRIOR FILING DATE: 2001-09-25
;  PRIOR APPLICATION NUMBER: US/09/964,824
;  PRIOR FILING DATE: 2001-09-27
;  PRIOR APPLICATION NUMBER: US/09/967,768
;  PRIOR FILING DATE: 2001-09-28
;  PRIOR APPLICATION NUMBER: US/09/968,007
;  PRIOR FILING DATE: 2001-10-02
;  PRIOR APPLICATION NUMBER: US/09/969,347
;  PRIOR FILING DATE: 2001-10-02
;  PRIOR APPLICATION NUMBER: US/09/969,708
;  PRIOR FILING DATE: 2001-10-03
;  Remaining Prior Application data removed - See File Wrapper or PALM.
;  NUMBER OF SEQ ID NOS: 8447
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 7205
;   LENGTH: 1855
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)..(1855)
;   OTHER INFORMATION: n=a,t,g or c
US-10-843-641A-7205

  Query Match             84.6%;  Score 1450;  DB 21;  Length 1855;
  Best Local Similarity   91.7%;  Pred. No. 0;
  Matches 1568;  Conservative    0;  Mismatches  135;  Indels    7;  Gaps    3;

Qy          4 GCATTGCACCAGGATGACTCTGAAATGGACTTCAGTTCTTCTGCTGATACATCTCCAGTT 63
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Db          2 GCATTGCACCAGGATGTCTGTGAAATGGACTTCAGTAATTTTGCTAATACAACTG-AGCT 60

Qy         64 GTTACTTTAGCTCTGGGAGTTGTGGAAAAGTGCTGGTGTGGGCCGCAGAATACAGCCATT 123
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Db         61 TTTGCTTTAGCTCTGGGAATTGTGGAAAGGTGCTGGTGTGGGCAGCAGAATACAGCCATT 120

Qy        124 GGATGAATATGAAGACAATCCTGAAAGAGCTTGTTCAGAGAGGTCATGAGGTGACTGTAC 183
              |||||||||| |||||||||||| | |||||| ||||||||||||||||||||||||||||
Db        121 GGATGAATATAAAGACAATCCTGGATGAGCTTATTCAGAGAGGTCATGAGGTGACTGTAC 180

Qy        184 TGGCATCTTCAGCTTCCATTCTTTTTGATCCCAATGATGCATCCACTCTTAAATTTGAAG 243
              |||||||||||||||||||||||||||||||  |  ||||| |||||||| |||||
Db        181 TGGCATCTTCAGCTTCCATTCTTTTTGATCCCAACAACTCATCCGCTCTTAAAATTGAAA 240

Qy        244 TTTATCCTACATCTTTAACTAAAACTGAATTTGAGAATATCATCATGCAACAGGTTAAGA 303
              |||||||||||||||||||||||| || ||||||| |||||||||||||| ||||||
Db        241 TTTATCCCACATCTTTAACTAAAACTGAGTTGGAGAATTTCATCATGCAACAGATTAAGA 300

Qy        304 GATGGTCAGACATTCGAAAAGATAGCTTTTGGTTATATTTTTCACAAGAACAAGAAATCC 363
              |||||||||| ||| ||||||||  |||||||||||||||||||||| ||| ||||||
Db        301 GATGGTCAGACCTTCCAAAAGATACATTTTGGTTATATTTTTCACAAGTACAGGAAATCA 360

Qy        364 TGTGGGAATTATATGACATATTTAGAAACTTCTGTAAAGATGTAGTTTCAAATAAGAAAG 423
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Db        361 TGTCAATATTTGGTGACATAACTAGAAAGTTCTGTAAAGATGTAGTTTCAAATAAGAAAT 420

Qy        424 TTATGAAAAAACTACAAGAGTCAAGATTTGACATCGTTTTTGCAGATGCTGTTTTTCCCT 483
              |||||||||| |||||||||||||||||||| || |||||||||||||| |||||||||
Db        421 TTATGAAAAAAGTACAAGAGTCAAGATTTGACGTCATTTTTGCAGATGCTATTTTTCCCT 480

Qy        484 GTGGTGAGCTGCTGGCTGCGCTACTTAACATACGGTTTGTGTACAGTCTCCGCTTTACTC 543
              || |||||||||||||||| |||| |||||||||  ||||||||||||||| |||| |||
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Qy        544 CTGGCTACACAATTGAAAGGCACAGTGGAGGACTGATTTTCCCTCCTTCCTACATACCTA 603
              |||||||||  |||||| ||| ||||||||| | ||||||||||||||||||| |||||
Db        541 CTGGCTACACTTTTGAAAAGCATAGTGGAGGATTTATTTTCCCTCCTTCCTACGTACCTG 600

Qy        604 TTGTTATGTCAAAATTAAGTGATCAAATGACTTTCATGGAGAGGGTAAAAAATATGATCT 663
              |||||||||| |||||| ||||||||||||||||||||||||||||||||||||||||
Db        601 TTGTTATGTCAGAATTAACTGATCAAATGACTTTCATGGAGAGGGTAAAAAATATGATCT 660

Qy        664 ATGTGCTTTATTTTGACTTTTGGTTCCAAATGTCTGATATGAAGAAGTGGGATCAGTTTT 723
              |||||||||| |||||||||||||||| |||| | ||| ||||||||||||||||||||
Db        661 ATGTGCTTTACTTTGACTTTTGGTTCGAAATATTTGACATGAAGAAGTGGGATCAGTTTT 720

Qy        724 ACAGTGAAGTTTTAGGAAGACCCACTACCTTATTTGAGACAATGGGAAAAGCTGACATAT 783
              | |||||||| |||||||||||||||| |||| |||||||||||| ||||||||| |||
Db        721 ATAGTGAAGTTCTAGGAAGACCCACTACGTTATCTGAGACAATGGGGAAAGCTGACGTAT 780

Qy        784 GGCTTATGCGAAACTCCTGGAGTTTTCAATTTCCTCATCCATTCTTACCAAACGTTGATT 843
              ||||||| |||||||||||| |||||| |||||||||||| |||||||||| |||||||
Db        781 GGCTTATTCGAAACTCCTGGAATTTTCAGTTTCCTCATCCACTCTTACCAAATGTTGATT 840

Qy        844 TTGTTGGAGGATTCCACTGGCAAACCTGCCAAACCCCTACCTAAGGAAATGGAGGAGTTT 903
              |||||||||| |||||| |||||||||||||||||||| |||||||||||||| || |||
Db        841 TTGTTGGAGGACTCCACT-GCAAACCTGCCAAACCCCTGCCTAAGGAAATGGAAGACTTT 899

Qy        904 GTACAGAGCTCTGGAGAAAATGGTGTTGTGGTGTTTTCTCTGGGGTCAGTGATAAGTAAC 963
              |||||||||||||||||||||||||||||||||||||||||||||||||| || | ||||||
Db        900 GTACAGAGCTCTGGAGAAAATGGTGTTGTGGTGTTTTCTCTGGGGTCAATGGTCAGTAAC 959

Qy        964 ATGACAGCAGAAAGGGCCAATGTAATTGCAACAGCCCTTGCCAAGATCCCACAAAAGGTT 1023
              ||||||| |||||||||||| ||||||||| ||||||| ||| ||||||||||||||||||
Db        960 ATGACAGAAGAAAGGGCCAACGTAATTGCATCAGCCCTGGCCCAGATCCCACAAAAGGTT 1019

Qy       1024 CTGTGGAGATTTGATGGGAATAAACCAGATGCCTTAGGTCTCAATACTCGGCTGTATAAG 1083
              ||||||||||||||||||||||||||||||||||| |||||||||||||||||||||||||
Db       1020 CTGTGGAGATTTGATGGGAATAAACCAGATACCTTAGGTCTCAATACTCGGCTGTATAAG 1079

Qy       1084 TGGATACCCCAGAATGACCTTCTAGGTCATCCAAAAACCAGAGCTTTTATAACTCATGGT 1143
              |||||||||||||||||||||||||||||||||||| ||||||||||||||||||||||||
Db       1080 TGGATACCCCAGAATGACCTTCTAGGTCATCCAAAGACCAGAGCTTTTATAACTCATGGT 1139

Qy       1144 GGAGCCAATGGCATCTATGAGGCAATCTACCATGGGATCCCTATGGTGGGCATTCCATTG 1203
              |||||||||||||||| ||||||||||||||||||||||||||||||| |||||||||
Db       1140 GGAGCCAATGGCATCTACGAGGCAATCTACCATGGGATCCCTATGGTGGGGATTCCATTG 1199

Qy       1204 TTTTGGGATCAACCTGATAACATTGCTCACATGAAGGCCAAGGGAGCAGCTGTTAGATTG 1263
              |||   |||||||||||||||||||||||||||||||||||||||||||||||||||| ||
Db       1200 TTTGCCGATCAACCTGATAACATTGCTCACATGAAGGCCAGGGGAGCAGCTGTTAGAGTG 1259

Qy       1264 GACTTCAACACAATGTCGAGTACAGACCTGCTGAATGCACTGAAGACAGTAATTAATGAT 1323
              |||||||||||||||||||||||||||| |||||||||| |||||| ||||||||||||
Db       1260 GACTTCAACACAATGTCGAGTACAGACTTGCTGAATGCATTGAAGAGAGTAATTAATGAT 1319

Qy       1324 CCTTTATATAAAGAGAATATTATGAAATTATCAAGAATTCAACATGATCAACCAGTAAAG 1383
              |||| |||||||||||| ||||||||||||||||||||||||||||||||||||| |||
Db       1320 CCTTCATATAAAGAGAATGTTATGAAATTATCAAGAATTCAACATGATCAACCAGTGAAG 1379
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Qy       1384 CCCCTGGATCGAGCAGTCTTCTGGATTGAATTTGTCATGCCCCACAAAGGAGCCAAACAC 1443
             ||||||||||||||||||||||||||||||||||||||||||| |||||||||||| ||||||
Db       1380 CCCCTGGATCGAGCAGTCTTCTGGATTGAATTTGTCATGCGCCACAAAGGAGCTAAACAC 1439

Qy       1444 CTTCGAGTTGCAGCCCATGACCTCACCTGGTTCCAGTACCACTCTTTGGATGTGATTGGG 1503
             |||||  |||||||||||| ||||||||||||||||||||||||||||||||||||||||||
Db       1440 CTTCGGGTTGCAGCCCACGACCTCACCTGGTTCCAGTACCACTCTTTGGATGTGATTGGG 1499

Qy       1504 TTTCTGCTGGCCTGTGTGGCAACTGTGATATTTATCATCACAAAGTTTTGTCTGTTTTGT 1563
             ||  |||||||  |||||||||||||||||||||||||||||  |||||||  | ||||||||||||
Db       1500 TTCCTGCTGGTCTGTGTGGCAACTGTGATATTTATCGTCACAAAATGTTGTCTGTTTTGT 1559

Qy       1564 TTCTGGAAGTTTGCTAGAAAAGGGAAGAAGGGAAAAAGAGATTAGTTATGTCTGACATTT 1623
             ||||||||||||||||||||||  ||||||||||||  ||||||||| |||||  ||||
Db       1560 TTCTGGAAGTTTGCTAGAAAAGCAAAGAAGGGAAAAAATGATTAGTTATATCTGAGATTT 1619

Qy       1624 GAAGCTGGAAAACCAGATAGATAGGACAACTTCAGTTTATTCCAGCAAGAAAGAAAAGAT 1683
             |||||||||||||| |||||  |  ||| ||||||||||||||||||||      ||||||
Db       1620 GAAGCTGGAAAACCTGATAGGTGAGACTACTTCAGTTTATTCCAGCAAG-----AAAGAT 1674

Qy       1684 TGTTATGCAAGATTTCTTTCTTCCTGTGAC 1713
             ||| ||||||||||||||||||| |||
Db       1675 TGTGATGCAAGATTTCTTTCTTCCTGAGAC 1704
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RESULT 12
US-10-205-522-39
; Sequence 39, Application US/10205522
; Publication No. US20030077629A1
; GENERAL INFORMATION:
;  APPLICANT: Penny, Laura
;  APPLICANT:  Galvin, Margaret
;  APPLICANT:  Miller, Andrew
;  APPLICANT:  Reidy, Michael
;  TITLE OF INVENTION: Genotyping Human
;  TITLE OF INVENTION:  UDP-Glucuronosyltransferase 2B4 (UGT2B4), 2B7 (UGT2B7) and
;  TITLE OF INVENTION:  2B15 (UGT2B15) Genes
;  FILE REFERENCE: SEQ-22PRV2
;  CURRENT APPLICATION NUMBER: US/10/205,522
;  CURRENT FILING DATE:  2002-07-24
;  PRIOR APPLICATION NUMBER: US/09/356,806
;  PRIOR FILING DATE: 1999-07-20
;  NUMBER OF SEQ ID NOS: 164
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 39
;   LENGTH: 1854
;   TYPE: DNA
;   ORGANISM: H. sapiens
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (15)...(1584)
US-10-205-522-39

  Query Match             84.3%;  Score 1443.6;  DB 14;  Length 1854;
  Best Local Similarity   91.5%;  Pred. No. 0;
  Matches 1564;  Conservative    0;  Mismatches  139;  Indels    7;  Gaps    3;
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Qy          4 GCATTGCACCAGGATGACTCTGAAATGGACTTCAGTTCTTCTGCTGATACATCTCCAGTT 63
              |||||||||||||||| || |||||||||||||||  || |||| ||||| ||  || |
Db          2 GCATTGCACCAGGATGTCTGTGAAATGGACTTCAGTAATTTTGCTAATACAACTG-AGCT 60

Qy         64 GTTACTTTAGCTCTGGGAGTTGTGGAAAAGTGCTGGTGTGGGCCGCAGAATACAGCCATT 123
               || |||||||||||||| |||||||| |||||||||||||| ||||||||||||||||
Db         61 TTTGCTTTAGCTCTGGGAATTGTGGAAAGGTGCTGGTGTGGGCAGCAGAATACAGCCATT 120

Qy        124 GGATGAATATGAAGACAATCCTGAAAGAGCTTGTTCAGAGAGGTCATGAGGTGACTGTAC 183
              |||||||||| |||||||||||  | ||||| ||||||||||||||||||||||||||||
Db        121 GGATGAATATAAAGACAATCCTGGATGAGCTTATTCAGAGAGGTCATGAGGTGACTGTAC 180

Qy        184 TGGCATCTTCAGCTTCCATTCTTTTTGATCCCAATGATGCATCCACTCTTAAATTTGAAG 243
              |||||||||||||||||||||||||||||||  |  ||||| |||||||| |||||
Db        181 TGGCATCTTCAGCTTCCATTCTTTTTGATCCCAACAACTCATCCGCTCTTAAAATTGAAA 240
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Qy        244 TTTATCCTACATCTTTAACTAAAACTGAATTTGAGAATATCATCATGCAACAGGTTAAGA 303
              ||||||| |||||||||||||||||||| || |||||| ||||||||||||||| ||||||
Db        241 TTTATCCCACATCTTTAACTAAAACTGAGTTGGAGAATTTCATCATGCAACAGATTAAGA 300

Qy        304 GATGGTCAGACATTCGAAAAGATAGCTTTTGGTTATATTTTTCACAAGAACAAGAAATCC 363
              |||||||||| ||| |||||||| |||||||||||||||||||||| ||| ||||||
Db        301 GATGGTCAGACCTTCCAAAAGATACATTTTGGTTATATTTTTCACAAGTACAGGAAATCA 360

Qy        364 TGTGGGAATTATATGACATATTTAGAAACTTCTGTAAAGATGTAGTTTCAAATAAGAAAG 423
              |||   |||   |||||||  |||||| ||||||||||||||||||||||||||||||
Db        361 TGTCAATATTTGGTGACATAACTAGAAAGTTCTGTAAAGATGTAGTTTCAAATAAGAAAT 420

Qy        424 TTATGAAAAAACTACAAGAGTCAAGATTTGACATCGTTTTTGCAGATGCTGTTTTTCCCT 483
              |||||||||| |||||||||||||||||||| || |||||||||||| |||||||||
Db        421 TTATGAAAAAAGTACAAGAGTCAAGATTTGACGTCATTTTTGCAGATGCTATTTTTCCCT 480

Qy        484 GTGGTGAGCTGCTGGCTGCGCTACTTAACATACGGTTTGTGTACAGTCTCCGCTTTACTC 543
              || |||||||||||||| |||| |||||||||  |||||||||||||| ||||  |||
Db        481 GTAGTGAGCTGCTGGCTGAGCTATTTAACATACCCTTTGTGTACAGTCTCAGCTTCTCTC 540

Qy        544 CTGGCTACACAATTGAAAGGCACAGTGGAGGACTGATTTTCCCTCCTTCCTACATACCTA 603
              |||||||||  |||||| ||| |||||||||  | ||||||||||||||||||  ||||||
Db        541 CTGGCTACACTTTTGAAAAGCATAGTGGAGGATTTATTTTCCCTCCTTCCTACGTACCTG 600

Qy        604 TTGTTATGTCAAAATTAAGTGATCAAATGACTTTCATGGAGAGGGTAAAAAATATGATCT 663
              |||||||||||  ||||||  ||||||||||||||||||||||||||||||||||||||||
Db        601 TTGTTATGTCAGAATTAACTGATCAAATGACTTTCATGGAGAGGGTAAAAAATATGATCT 660

Qy        664 ATGTGCTTTATTTTGACTTTTGGTTCCAAATGTCTGATATGAAGAAGTGGGATCAGTTTT 723
              |||||||||| |||||||||||||| |||| | ||| ||||||||||||||||||||||
Db        661 ATGTGCTTTACTTTGACTTTTGGTTCGAAATATTTGACATGAAGAAGTGGGATCAGTTTT 720

Qy        724 ACAGTGAAGTTTTAGGAAGACCCACTACCTTATTTGAGACAATGGGAAAAGCTGACATAT 783
              | |||||||| |||||||||||||| |||| |||||||||||| |||||||| |||
Db        721 ATAGTGAAGTTCTAGGAAGACCCACTACATTATCTGAGACAATGGGGAAAGCTGACGTAT 780

Qy        784 GGCTTATGCGAAACTCCTGGAGTTTTCAATTTCCTCATCCATTCTTACCAAACGTTGATT 843
              ||||||| |||||||||||||| |||||| |||||  ||||| |||||||||| |||||||
Db        781 GGCTTATTCGAAACTCCTGGAATTTTCAGTTTCCATATCCACTCTTACCAAATGTTGATT 840

Qy        844 TTGTTGGAGGATTCCACTGGCAAACCTGCCAAACCCCTACCTAAGGAAATGGAGGAGTTT 903
              |||||||||| |||||| |||||||||||||||||| |||||||||||||| || |||
Db        841 TTGTTGGAGGACTCCACT-GCAAACCTGCCAAACCCCTGCCTAAGGAAATGGAAGACTTT 899

Qy        904 GTACAGAGCTCTGGAGAAAATGGTGTTGTGGTGTTTTCTCTGGGGTCAGTGATAAGTAAC 963
              |||||||||||||||||||||||||||||||||||||||||||||||||| || | ||||||
Db        900 GTACAGAGCTCTGGAGAAAATGGTGTTGTGGTGTTTTCTCTGGGGTCAATGGTCAGTAAC 959

Qy        964 ATGACAGCAGAAAGGGCCAATGTAATTGCAACAGCCCTTGCCAAGATCCCACAAAAGGTT 1023
              ||||||| |||||||||||  |||||||| ||||||| ||| ||||||||||||||||||
Db        960 ATGACAGAAGAAAGGGCCAACGTAATTGCATCAGCCCTGGCCCAGATCCCACAAAAGGTT 1019

Qy       1024 CTGTGGAGATTTGATGGGAATAAACCAGATGCCTTAGGTCTCAATACTCGGCTGTATAAG 1083
              |||||||||||||||||||||||||||||||||||||||||||||||||| || |||
Db       1020 CTGTGGAGATTTGATGGGAATAAACCAGATACCTTAGGTCTCAATACTCGGCTCTACAAG 1079

Qy       1084 TGGATACCCCAGAATGACCTTCTAGGTCATCCAAAAACCAGAGCTTTTATAACTCATGGT 1143
              |||||||||||||||||||||||||||||||||| ||||||||||||||||||||||||
Db       1080 TGGATACCCCAGAATGACCTTCTAGGTCATCCAAAGACCAGAGCTTTTATAACTCATGGT 1139

Qy       1144 GGAGCCAATGGCATCTATGAGGCAATCTACCATGGGATCCCTATGGTGGGCATTCCATTG 1203
              |||||||||||||||| |||||||||||||||||||||||||||||| |||||||||
Db       1140 GGAGCCAATGGCATCTACGAGGCAATCTACCATGGGATCCCTATGGTGGGGATTCCATTG 1199

Qy       1204 TTTTGGGATCAACCTGATAACATTGCTCACATGAAGGCCAAGGGAGCAGCTGTTAGATTG 1263
              |||  |||||||||||||||||||||||||||||||||||||||||||||||||||| ||
Db       1200 TTTGCCGATCAACCTGATAACATTGCTCACATGAAGGCCAGGGGAGCAGCTGTTAGAGTG 1259

Qy       1264 GACTTCAACACAATGTCGAGTACAGACCTGCTGAATGCACTGAAGACAGTAATTAATGAT 1323
              |||||||||||||||||||||||||||||||| |||||||||| |||||| ||||||||||||
Db       1260 GACTTCAACACAATGTCGAGTACAGACTTGCTGAATGCATTGAAGAGAGTAATTAATGAT 1319

Qy       1324 CCTTTATATAAAGAGAATATTATGAAATTATCAAGAATTCAACATGATCAACCAGTAAAG 1383
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Db       1320 CCTTCATATAAAGAGAATGTTATGAAATTATCAAGAATTCAACATGATCAACCAGTGAAG 1379

Qy       1384 CCCCTGGATCGAGCAGTCTTCTGGATTGAATTTGTCATGCCCCACAAAGGAGCCAAACAC 1443

Db       1380 CCCCTGGATCGAGCAGTCTTCTGGATTGAATTTGTCATGCGCCACAAAGGAGCTAAACAC 1439

Qy       1444 CTTCGAGTTGCAGCCCATGACCTCACCTGGTTCCAGTACCACTCTTTGGATGTGATTGGG 1503

Db       1440 CTTCGGGTTGCAGCCCACGACCTCACCTGGTTCCAGTACCACTCTTTGGATGTGATTGGG 1499

Qy       1504 TTTCTGCTGGCCTGTGTGGCAACTGTGATATTTATCATCACAAAGTTTTGTCTGTTTTGT 1563

Db       1500 TTCCTGCTGGTCTGTGTGGCAACTGTGATATTTATCGTCACAAAATGTTGTCTGTTTTGT 1559

Qy       1564 TTCTGGAAGTTTGCTAGAAAAGGGAAGAAGGGAAAAAGAGATTAGTTATGTCTGACATTT 1623

Db       1560 TTCTGGAAGTTTGCTAGAAAAGCAAAGAAGGGAAAAAATGATTAGTTATATCTGAGATTT 1619

Qy       1624 GAAGCTGGAAAACCAGATAGATAGGACAACTTCAGTTTATTCCAGCAAGAAAGAAAAGAT 1683

Db       1620 GAAGCTGGAAAACCTGATAGGTGAGACTACTTCAGTTTATTCCAGCAAG-----AAAGAT 1674

Qy       1684 TGTTATGCAAGATTTCTTTCTTCCTGTGAC 1713

Db       1675 TGTGATGCAAGATTTCTTTCTTCCTGAGAC 1704


RESULT 13
US-09-981-353-193
; Sequence 193, Application US/09981353
; Patent No. US20020160382A1
; GENERAL INFORMATION:
;  APPLICANT: Lasek, Amy W.
;  APPLICANT:  Jones, David A.
;  TITLE OF INVENTION: GENES EXPRESSED IN COLON CANCER
;  FILE REFERENCE: PA-0038 US
;  CURRENT APPLICATION NUMBER: US/09/981,353
;  CURRENT FILING DATE:  2001-10-11
;  NUMBER OF SEQ ID NOS: 194
;  SOFTWARE: PERL Program
; SEQ ID NO 193
;   LENGTH: 1714
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   OTHER INFORMATION: Incyte ID No. US20020160382A1 088078CB1
US-09-981-353-193

  Query Match             83.9%;  Score 1436.4;  DB 9;  Length 1714;
  Best Local Similarity   91.3%;  Pred. No. 0;
  Matches 1558;  Conservative    0;  Mismatches  141;  Indels    7;  Gaps    3;

Qy          1 ATCGCATTGCACCAGGATGACTCTGAAATGGACTTCAGTTCTTCTGCTGATACATCTCCA 60

Db         16 ATTGCATTGCACCAGGATGTCTGTGAAATGGACTTCAGTAATTTTGCTAATACAACT-GA 74

Qy         61 GTTGTTACTTTAGCTCTGGGAGTTGTGGAAAAGTGCTGGTGTGGGCCGCAGAATACAGCC 120

Db         75 GCTTTTGCTTTAGCTCTGGGAATTGTGGAAAGGTGCTGGTGTGGGCAGCAGAATACAGCC 134

Qy        121 ATTGGATGAATATGAAGACAATCCTGAAAGAGCTTGTTCAGAGAGGTCATGAGGTGACTG 180

Db        135 ATTGGATGAATATAAAGACAATCCTGGATGAGCTTATTCAGAGAGGTCATGAGGTGACTG 194

Qy        181 TACTGGCATCTTCAGCTTCCATTCTTTTTGATCCCAATGATGCATCCACTCTTAAATTTG 240

Db        195 TACTGGCATCTTCAGCTTCCATTCTTTTTGATCCCAACAACTCATCCGCTCTTAAAATTG 254

Qy        241 AAGTTTATCCTACATCTTTAACTAAAACTGAATTTGAGAATATCATCATGCAACAGGTTA 300

Db        255 AAATTTATCCCACATCTTTAACTAAAACTGAGTTGGAGAATTTCATCATGCAACAGATTA 314

Qy        301 AGAGATGGTCAGACATTCGAAAAGATAGCTTTTGGTTATATTTTTCACAAGAACAAGAAA 360

Db        315 AGAGATGGTCAGACCTTCCAAAAGATACATTTTGGTTATATTTTTCACAAGTACAGGAAA 374

Qy        361 TCCTGTGGGAATTATATGACATATTTAGAAACTTCTGTAAAGATGTAGTTTCAAATAAGA 420

Db        375 TCATGTCAATATTTGGTGACATAACTAGAAAGTTCTGTAAAGATGTAGTTTCAAATAAGA 434

Qy        421 AAGTTATGAAAAAACTACAAGAGTCAAGATTTGACATCGTTTTTGCAGATGCTGTTTTTC 480

Db        435 AATTTATGAAAAAAGTACAAGAGTCAAGATTTGACGTCATTTTTGCAGATGCTATTTTTC 494

Qy        481 CCTGTGGTGAGCTGCTGGCTGCGCTACTTAACATACGGTTTGTGTACAGTCTCCGCTTTA 540

Db        495 CCTGTAGTGAGCTGCTGGCTGAGCTATTTAACATACCCTTTGTGTACAGTCTCAGCTTCT 554

Qy        541 CTCCTGGCTACACAATTGAAAGGCACAGTGGAGGACTGATTTTCCCTCCTTCCTACATAC 600

Db        555 CTCCTGGCTACACTTTTGAAAAGCATAGTGGAGGATTTATTTTCCCTCCTTCCTACGTAC 614

Qy        601 CTATTGTTATGTCAAAATTAAGTGATCAAATGACTTTCATGGAGAGGGTAAAAAATATGA 660

Db        615 CTGTTGTTATGTCAGAATTAACTGATCAAATGACTTTCATGGAGAGGGTAAAAAATATGA 674

Qy        661 TCTATGTGCTTTATTTTGACTTTTGGTTCCAAATGTCTGATATGAAGAAGTGGGATCAGT 720

Db        675 TCTATGTGCTTTACTTTGACTTTTGGTTCGAAATATTTGACATGAAGAAGTGGGATCAGT 734

Qy        721 TTTACAGTGAAGTTTTAGGAAGACCCACTACCTTATTTGAGACAATGGGAAAAGCTGACA 780

Db        735 TTTATAGTGAAGTTCTAGGAAGACCCACTACGTTATCTGAGACAATGGGGAAAGCTGACG 794

Qy        781 TATGGCTTATGCGAAACTCCTGGAGTTTTCAATTTCCTCATCCATTCTTACCAAACGTTG 840

Db        795 TATGGCTTATTCGAAACTCCTGGAATTTTCAGTTTCCTCATCCACTCTTACCAAATGTTG 854

Qy        841 ATTTTGTTGGAGGATTCCACTGGCAAACCTGCCAAACCCCTACCTAAGGAAATGGAGGAG 900

Db        855 ATTTTGTTGGAGGACTCCACT-GCAAACCTGCCAAACCCCTGCCTAAGGAAATGGAAGAC 913

Qy        901 TTTGTACAGAGCTCTGGAGAAAATGGTGTTGTGGTGTTTTCTCTGGGGTCAGTGATAAGT 960

Db        914 TTTGTACAGAGCTCTGGAGAAAATGGTGTTGTGGTGTTTTCTCTGGGGTCAATGGTCAGT 973

Qy        961 AACATGACAGCAGAAAGGGCCAATGTAATTGCAACAGCCCTTGCCAAGATCCCACAAAAG 1020

Db        974 AACATGACAGAAGAAAGGGCCAACGTAATTGCATCAGCCCTGGCCCAGATCCCACAAAAG 1033

Qy       1021 GTTCTGTGGAGATTTGATGGGAATAAACCAGATGCCTTAGGTCTCAATACTCGGCTGTAT 1080

Db       1034 GTTCTGTGGAGATTTGATGGGAATAAACCAGATACCTTAGGTCTCAATACTCGGCTCTAC 1093

Qy       1081 AAGTGGATACCCCAGAATGACCTTCTAGGTCATCCAAAAACCAGAGCTTTTATAACTCAT 1140

Db       1094 AAGTGGATACCCCAGAATGACCTTCTAGGTCATCCAAAGACCAGAGCTTTTATAACTCAT 1153

Qy       1141 GGTGGAGCCAATGGCATCTATGAGGCAATCTACCATGGGATCCCTATGGTGGGCATTCCA 1200

Db       1154 GGTGGAGCCAATGGCATCTACGAGGCAATCTACCATGGGATCCCTATGGTGGGGATTCCA 1213

Qy       1201 TTGTTTTGGGATCAACCTGATAACATTGCTCACATGAAGGCCAAGGGAGCAGCTGTTAGA 1260

Db       1214 TTGTTTGCTGATCAACCTGATAACATTGCTCACATGAAGGCCAGGGGAGCAGCTGTTAGA 1273

Qy       1261 TTGGACTTCAACACAATGTCGAGTACAGACCTGCTGAATGCACTGAAGACAGTAATTAAT 1320

Db       1274 GTGGACTTCAACACAATGTCGAGTACAGACTTGCTGAATGCATTGAAGAGAGTAATTAAT 1333

Qy       1321 GATCCTTTATATAAAGAGAATATTATGAAATTATCAAGAATTCAACATGATCAACCAGTA 1380

Db       1334 GATCCTTCATATAAAGAGAATGTTATGAAATTATCAAGAATTCAACATGATCAACCAGTG 1393
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Qy       1381 AAGCCCCTGGATCGAGCAGTCTTCTGGATTGAATTTGTCATGCCCCACAAAGGAGCCAAA 1440
             ||||||||||||||||||||||||||||||||||||||||||| |||||||||||| |||
Db       1394 AAGCCCCTGGATCGAGCAGTCTTCTGGATTGAATTTGTCATGCGCCACAAAGGAGCTAAA 1453

Qy       1441 CACCTTCGAGTTGCAGCCCATGACCTCACCTGGTTCCAGTACCACTCTTTGGATGTGATT 1500
             |||||||| |||||||||| ||||||||||||||||||||||||||||||||||||||||
Db       1454 CACCTTCGGGTTGCAGCCCACGACCTCACCTGGTTCCAGTACCACTCTTTGGATGTGATT 1513

Qy       1501 GGGTTTCTGCTGGCCTGTGTGGCAACTGTGATATTTATCATCACAAAGTTTTGTCTGTTT 1560
             ||||| ||||||| |||||||||||||||||||||||| ||||||| | ||||||||||
Db       1514 GGGTTCCTGCTGGTCTGTGTGGCAACTGTGATATTTATCGTCACAAAATGTTGTCTGTTT 1573

Qy       1561 TGTTTCTGGAAGTTTGCTAGAAAAGGGAAGAAGGGAAAAAGAGATTAGTTATGTCTGACA 1620
             |||||||||||||||||||||||  ||||||||||||  ||||||||| ||||| |
Db       1574 TGTTTCTGGAAGTTTGCTAGAAAAGCAAAGAAGGGAAAAAATGATTAGTTATATCTGAGA 1633

Qy       1621 TTTGAAGCTGGAAAACCAGATAGATAGGACAACTTCAGTTTATTCCAGCAAGAAAGAAAA 1680
             |||||||||||||||| ||||| |  ||| ||||||||||||||||||||     |||
Db       1634 TTTGAAGCTGGAAAACCTGATAGGTGAGACTACTTCAGTTTATTCCAGCAAG-----AAA 1688

Qy       1681 GATTGTTATGCAAGATTTCTTTCTTC 1706
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Db       1689 GATTGTGATGCATGATGTCGATCTTC 1714
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RESULT 14
US-10-468-125-18
; Sequence 18, Application US/10468125
; Publication No. US20040082061A1
; GENERAL INFORMATION:
;  APPLICANT: ASTROMOFF, Anna
;  APPLICANT:  AU-YOUNG, Janice
;  APPLICANT:  BAUGHN, Mariah R.
;  APPLICANT:  DING, Li
;  APPLICANT:  DUGGAN, Brendan M.
;  APPLICANT:  FORSYTHE, Ian J.
;  APPLICANT:  GIETZEN, Kimberly J.
;  APPLICANT:  GRIFFIN, Jennifer A.
;  APPLICANT:  LEE, Ernestine A.
;  APPLICANT:  LU, Yan
;  APPLICANT:  RICHARDSON, Thomas W.
;  APPLICANT:  RING, Huijun Z.
;  APPLICANT:  SANJANWALA, Madhusudan
;  APPLICANT:  SWARNAKAR, Anita
;  APPLICANT:  CHAWLA, Narinder K.
;  APPLICANT:  WARREN, Bridget A.
;  APPLICANT:  XU, Yuming
;  APPLICANT:  YUE, Henry
;  APPLICANT:  ZEBARJADIAN, Yeganeh
;  TITLE OF INVENTION: DRUG METABOLIZING ENZYMES
;  FILE REFERENCE: PI-0363 USN
;  CURRENT APPLICATION NUMBER: US/10/468,125
;  CURRENT FILING DATE:  2003-08-15
;  PRIOR APPLICATION NUMBER: PCT/US02/04918
;  PRIOR FILING DATE: 2002-02-14
;  PRIOR APPLICATION NUMBER: US 60/269,643
;  PRIOR FILING DATE: 2001-02-16
;  PRIOR APPLICATION NUMBER: US 60/271,332
;  PRIOR FILING DATE: 2001-02-23
;  PRIOR APPLICATION NUMBER: US 60/276,767
;  PRIOR FILING DATE: 2001-03-16
;  PRIOR APPLICATION NUMBER: US 60/282,077
;  PRIOR FILING DATE: 2001-04-06
;  PRIOR APPLICATION NUMBER: US 60/285,447
;  PRIOR FILING DATE: 2001-04-19
;  PRIOR APPLICATION NUMBER: US 60/287,060
;  PRIOR FILING DATE: 2001-04-27
;  PRIOR APPLICATION NUMBER: US 60/288,543
;  PRIOR FILING DATE: 2001-05-03
;  NUMBER OF SEQ ID NOS: 24
;  SOFTWARE: PERL Program
; SEQ ID NO 18
;   LENGTH: 1639
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   OTHER INFORMATION: Incyte ID No: 7493833CB1
US-10-468-125-18

  Query Match             80.2%;  Score 1374;  DB 18;  Length 1639;
  Best Local Similarity   91.0%;  Pred. No. 0;
  Matches 1494;  Conservative    0;  Mismatches  145;  Indels    3;  Gaps    3;

Qy         17 ATGACTCTGAAATGGACTTCAGTTCTTCTGCTGATACATCTCCAGTTGTTACTTTAGCTC 76
              ||| || |||||||||||||| |||||||||||||| ||  || ||||||||||||||
Db          1 ATGTCTATGAAATGGACTTCAGCTCTTCTGCTGATACAGCTG-AGCTGTTACTTTAGCTC 59

Qy         77 TGGGAGTTGTGGAAAAGTGCTGGTGTGGGCCGCAGAATACAGCCATTGGATGAATATGAA 136
              |||||||||||||||| |||||||||||| || |||||| |||||| |||||||||||| ||
Db         60 TGGGAGTTGTGGAAAGGTGCTGGTGTGGCCCACAGAATTCAGCCACTGGATGAATATAAA 119

Qy        137 GACAATCCTGAAAGAGCTTGTTCAGAGAGGTCATGAGGTGACTGTACTGGCATCTTCAGC 196
              |||||||||| | || ||||| |||||||||||||||||||||||| ||||||||||||
Db        120 GACAATCCTGGATGAACTTGTCCAGAGAGGTCATGAGGTGACTGTATTGGCATCTTCAGC 179

Qy        197 TTCCATTCTTTTTGATCCCAATGATGCATCCACTCTTAAATTTGAAGTTTATCCTACATC 256
              |||||||  ||| ||||||||     |||| |||||||||||||||||||||||  |||
Db        180 TTCCATTTCTTTCGATCCCAACAGCCCATCTACTCTTAAATTTGAAGTTTATCCTGTATC 239

Qy        257 TTTAACTAAAACTGAATTTGAGAATATCATCATGCAACAGGTTAAGAGATGGTCAGACAT 316
              |||||||||||||||| |||||| |||| |||| ||| | ||||||||||||| |||| |
Db        240 TTTAACTAAAACTGAGTTTGAGGATATTATCAAGCAGCTGGTTAAGAGATGGGCAGAACT 299

Qy        317 TCGAAAAGATAGCTTTTGGTTATATTTTTCACAAGAACAAGAAATCCTGTGGGAATTATA 376
              || |||||| |  |||||||| |||||||||||||| |||||||||| |||||  |||  |
Db        300 TCCAAAAGACACATTTTGGTCATATTTTTCACAAGTACAAGAAATCATGTGGACATTTAA 359

Qy        377 TGACATATTTAGAAACTTCTGTAAAGATGTAGTTTCAAATAAGAAAGTTATGAAAAAACT 436
              ||||||| ||||||| |||||||| ||| |||||||||||||||| ||||||| |||||
Db        360 TGACATACTTAGAAAGTTCTGTAAGGATATAGTTTCAAATAAGAAACTTATGAAGAAACT 419

Qy        437 ACAAGAGTCAAGATTTGACATCGTTTTTGCAGATGCTGTTTTTCCCTGTGGTGAGCTGCT 496
              ||| |||||||||||||| || |||||||||||| |||||||||| ||||||||||
Db        420 ACAGGAGTCAAGATTTGACGTCATTTTTGCAGATGCTATTTTTCCCTGTAGTGAGCTGCT 479

Qy        497 GGCTGCGCTACTTAACATACGGTTTGTGTACAGTCTCCGCTTTACTCCTGGCTACACAAT 556
              ||||| |||| |||||||||  |||||||||||||||| ||||  ||||||||||||  |
Db        480 GGCTGAGCTATTTAACATACCCTTTGTGTACAGTCTCAGCTTCTCTCCTGGCTACACTTT 539

Qy        557 TGAAAGGCACAGTGGAGGACTGATTTTCCCTCCTTCCTACATACCTATTGTTATGTCAAA 616
              ||||| ||| |||||||||| | |||||||||||||||||| ||||| |||||||||| |
Db        540 TGAAAAGCATAGTGGAGGATTTATTTTCCCTCCTTCCTACGTACCTGTTGTTATGTCAGA 599

Qy        617 ATTAAGTGATCAAATGACTTTCATGGAGAGGGTAAAAAATATGATCTATGTGCTTTATTT 676
              ||||| ||||||||||||||||||||||||||||||||||||||||||||||||||| ||
Db        600 ATTAACTGATCAAATGACTTTCATGGAGAGGGTAAAAAATATGATCTATGTGCTTTACTT 659

Qy        677 TGACTTTTGGTTCCAAATGTCTGATATGAAGAAGTGGGATCAGTTTTACAGTGAAGTTTT 736
              |||||||||||| |||| | ||| |||||||||||||||||||||| ||||||||| |
Db        660 TGACTTTTGGTTCGAAATATTTGACATGAAGAAGTGGGATCAGTTTTATAGTGAAGTTCT 719

Qy        737 AGGAAGACCCACTACCTTATTTGAGACAATGGGAAAAGCTGACATATGGCTTATGCGAAA 796
              |||||||||||||| |||| |||||||||||| |||||||||| |||||||||| |||||
Db        720 AGGAAGACCCACTACATTATCTGAGACAATGGGGAAAGCTGACGTATGGCTTATTCGAAA 779

Qy        797 CTCCTGGAGTTTTCAATTTCCTCATCCATTCTTACCAAACGTTGATTTTGTTGGAGGATT 856
              |||||||| |||||| |||||||||||| |||||||||| |||||||||||||||||| |
Db        780 CTCCTGGAATTTTCAGTTTCCTCATCCACTCTTACCAAATGTTGATTTTGTTGGAGGACT 839

Qy        857 CCACTGGCAAACCTGCCAAACCCCTACCTAAGGAAATGGAGGAGTTTGTACAGAGCTCTG 916
              ||||| |||||||||||||||||| |||||||||||||| || ||||||||||||||||
Db        840 CCACT-GCAAACCTGCCAAACCCCTGCCTAAGGAAATGGAAGACTTTGTACAGAGCTCTG 898

Qy        917 GAGAAAATGGTGTTGTGGTGTTTTCTCTGGGGTCAGTGATAAGTAACATGACAGCAGAAA 976
              |||||||||||||||||||||||||||||||||||| || | |||||||||||| |||||
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Db        899 GAGAAAATGGTGTTGTGGTGTTTTCTCTGGGGTCAATGGTCAGTAACATGACAGAAGAAA 958

Qy        977 GGGCCAATGTAATTGCAACAGCCCTTGCCAAGATCCCACAAAAGGTTCTGTGGAGATTTG 1036
              ||||||| |||||||| ||||||| ||| ||||||||||||||||||||||||||||||
Db        959 GGGCCAACGTAATTGCATCAGCCCTGGCCCAGATCCCACAAAAGGTTCTGTGGAGATTTG 1018

Qy       1037 ATGGGAATAAACCAGATGCCTTAGGTCTCAATACTCGGCTGTATAAGTGGATACCCCAGA 1096
              |||||||||||||||| |||||||||||||||||||| ||||||||||||||||
Db       1019 ATGGGAATAAACCAGATACCTTAGGTCTCAATACTCGGCTGTACAAGTGGATACCCCAGA 1078

Qy       1097 ATGACCTTCTAGGTCATCCAAAAACCAGAGCTTTTATAACTCATGGTGGAGCCAATGGCA 1156
              |||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||
Db       1079 ATGACCTTCTAGGTCATCCAAAGACCAGAGCTTTTATAACTCATGGTGGAGCCAATGGCA 1138

Qy       1157 TCTATGAGGCAATCTACCATGGGATCCCTATGGTGGGCATTCCATTGTTTTGGGATCAAC 1216
              |||| |||||||||||||||||||||||||||||||| ||||||||||||    |||||||
Db       1139 TCTACGAGGCAATCTACCATGGGATCCCTATGGTGGGGATTCCATTGTTTGCCGATCAAC 1198

Qy       1217 CTGATAACATTGCTCACATGAAGGCCAAGGGAGCAGCTGTTAGATTGGACTTCAACACAA 1276
              |||||||||||||||||||||||| |||||||||||||| ||||||||||||||
Db       1199 CTGATAACATTGCTCACATGAAGGCCAGGGGAGCAGCTGTTAGAGTGGACTTCAACACAA 1258

Qy       1277 TGTCGAGTACAGACCTGCTGAATGCACTGAAGACAGTAATTAATGATCCTTTATATAAAG 1336
              |||||||||||||| |||||||||| |||||| ||||||||||||||||| ||||||||
Db       1259 TGTCGAGTACAGACTTGCTGAATGCATTGAAGAGAGTAATTAATGATCCTTCATATAAAG 1318

Qy       1337 AGAATATTATGAAATTATCAAGAATTCAACATGATCAACCAGTAAAGCCCCTGGATCGAG 1396
              ||||| |||||||||||||||||||||||||||||||||||||||| ||||||||||||||||
Db       1319 AGAATGTTATGAAATTATCAAGAATTCAACATGATCAACCAGTGAAGCCCCTGGATCGAG 1378

Qy       1397 CAGTCTTCTGGATTGAATTTGTCATGCCCCACAAAGGAGCCAAACACCTTCGAGTTGCAG 1456
              |||||||||||||||||||||||||| |||||||||||| |||||||||||| |||||||
Db       1379 CAGTCTTCTGGATTGAATTTGTCATGCGCCACAAAGGAGCTAAACACCTTCGGGTTGCAG 1438

Qy       1457 CCCATGACCTCACCTGGTTCCAGTACCACTCTTTGGATGTGATTGGGTTTCTGCTGGCCT 1516
              |||| |||||||||||||||||||||||||||||||||||||||||||||||||| |||||| ||
Db       1439 CCCACGACCTCACCTGGTTCCAGTACCACTCTTTGGATGTGATTGGGTTCCTGCTGGTCT 1498

Qy       1517 GTGTGGCAACTGTGATATTTATCATCACAAAGTTTTGTCTGTTTTGTTTCTGGAAGTTTG 1576
              |||||||||||||||||| |||||||||| | |||||||||||||| ||||||||||||
Db       1499 GTGTGGCAACTGTGATATTCATCATCACAAAATGTTGTCTGTTTTGTGTCTGGAAGTTTG 1558

Qy       1577 CTAGAAAAGGGAAGAAGGGAAAAAGAGATTAGTTATGTCTGACATTTGAAGCTGGAAAAC 1636
              |||||  ||| |||||||| |||||||||| ||| ||||||    | ||||||||||||
Db       1559 TTAGAACAGGAAAGAAGGGGAAAAGAGATTAATTACGTCTGAGGCTGGAAGCTGGAAAA- 1617

Qy       1637 CAGATAGATAGGACAACTTCAG 1658
              | |||||  |  ||| |||||||
Db       1618 CTGATAGGTGAGACTACTTCAG 1639


RESULT 15
US-10-205-522-7
; Sequence 7, Application US/10205522
; Publication No. US20030077629A1
; GENERAL INFORMATION:
;  APPLICANT: Penny, Laura
;  APPLICANT:  Galvin, Margaret
;  APPLICANT:  Miller, Andrew
;  APPLICANT:  Reidy, Michael
;  TITLE OF INVENTION: Genotyping Human
;  TITLE OF INVENTION:  UDP-Glucuronosyltransferase 2B4 (UGT2B4), 2B7 (UGT2B7) and
;  TITLE OF INVENTION:  2B15 (UGT2B15) Genes
;  FILE REFERENCE: SEQ-22PRV2
;  CURRENT APPLICATION NUMBER: US/10/205,522
;  CURRENT FILING DATE:  2002-07-24
;  PRIOR APPLICATION NUMBER: US/09/356,806
;  PRIOR FILING DATE: 1999-07-20
;  NUMBER OF SEQ ID NOS: 164
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 7
;   LENGTH: 2092
;   TYPE: DNA
;   ORGANISM: H. sapiens
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (38)...(1621)
US-10-205-522-7

  Query Match             79.1%;  Score 1354.2;  DB 14;  Length 2092;
  Best Local Similarity   88.8%;  Pred. No. 0;
  Matches 1522;  Conservative    0;  Mismatches  183;  Indels    8;  Gaps    5;

Qy          1 ATCGCATTGCACCAGGATGACTCTGAAATGGACTTCAGTTCTTCTGCTGATACATCTCCA 60
              || |||||||| |||||| || ||||||||||||||| ||||||||||||||| || |
Db         22 ATTGCATTGCATCAGGATGTCTATGAAATGGACTTCAGCTCTTCTGCTGATACAGCT-GA 80

Qy         61 GTTGTTACTTTAGCTCTGGGAGTTGTGGAAAAGTGCTGGTGTGGGCCGCAGAATACAGCC 120
              | |||||||||||||||||||||||||||| |||||||||||| || |||||| |||||
Db         81 GCTGTTACTTTAGCTCTGGGAGTTGTGGAAAGGTGCTGGTGTGGCCCACAGAATTCAGCC 140

Qy        121 ATTGGATGAATATGAAGACAATCCTGAAAGAGCTTGTTCAGAGAGGTCATGAGGTGACTG 180
              | |||||||||| |||||||||||| | || ||||| ||||||||||||||||||||||
Db        141 ACTGGATGAATATAAAGACAATCCTGGATGAACTTGTCCAGAGAGGTCATGAGGTGACTG 200

Qy        181 TACTGGCATCTTCAGCTTCCATTCTTTTTGATCCCAATGATGCATCCACTCTTAAATTTG 240
              || |||||||||||||||||||||| ||| ||||||||     |||| ||||||||||||
Db        201 TATTGGCATCTTCAGCTTCCATTTCTTTCGATCCCAACAGCCCATCTACTCTTAAATTTG 260

Qy        241 AAGTTTATCCTACATCTTTAACTAAAACTGAATTTGAGAATATCATCATGCAACAGGTTA 300
              |||||||||||  |||||||||||||||||| |||||| |||| |||| ||| | |||||
Db        261 AAGTTTATCCTGTATCTTTAACTAAAACTGAGTTTGAGGATATTATCAAGCAGCTGGTTA 320

Qy        301 AGAGATGGTCAGACATTCGAAAAGATAGCTTTTGGTTATATTTTTCACAAGAACAAGAAA 360
              |||||||| ||||  ||| |||||| |  ||||||| |||||||||||||| ||||||||
Db        321 AGAGATGGGCAGAACTTCCAAAAGACACATTTTGGTCATATTTTTCACAAGTACAAGAAA 380

Qy        361 TCCTGTGGGAATTATATGACATATTTAGAAACTTCTGTAAAGATGTAGTTTCAAATAAGA 420
              || |||||  |||  |||||||| |||||||| |||||||| ||| ||||||||||||||
Db        381 TCATGTGGACATTTAATGACATACTTAGAAAGTTCTGTAAGGATATAGTTTCAAATAAGA 440

Qy        421 AAGTTATGAAAAAACTACAAGAGTCAAGATTTGACATCGTTTTTGCAGATGCTGTTTTTC 480
              || ||||||| |||||||| ||||||||||||||  | ||| |||||||||||||||| |
Db        441 AACTTATGAAGAAACTACAGGAGTCAAGATTTGATGTTGTTCTTGCAGATGCTGTTTTCC 500

Qy        481 CCTGTGGTGAGCTGCTGGCTGCGCTACTTAACATACGGTTTGTGTACAGTCTCCGCTTTA 540
              ||| |||||||||||||| | | ||||||| ||||  ||||| ||||| ||||||||
Db        501 CCTTTGGTGAGCTGCTGGCCGAGTTACTTAAAATACCCTTTGTCTACAGCCTCCGCTTCT 560

Qy        541 CTCCTGGCTACACAATTGAAAGGCACAGTGGAGGACTGATTTTCCCTCCTTCCTACATAC 600
              |||||||||| |||||||| ||| |||||||||||  | ||||||||||||  | |
Db        561 CTCCTGGCTACGCAATTGAAAAGCATAGTGGAGGACTTCTGTTCCCTCCTTCCTATGTGC 620

Qy        601 CTATTGTTATGTCAAAATTAAGTGATCAAATGACTTTCATGGAGAGGGTAAAAAATATGA 660
              || |||||||||| || ||||||| |||||||||||||| ||||||||||||||||||||
Db        621 CTGTTGTTATGTCAGAACTAAGTGACCAAATGACTTTCATAGAGAGGGTAAAAAATATGA 680

Qy        661 TCTATGTGCTTTATTTTGACTTTTGGTTCCAAATGTCTGATATGAAGAAGTGGGATCAGT 720
              |||||||||||||||||| |||||||||||||| | ||| ||||||||||||||||||||
Db        681 TCTATGTGCTTTATTTTGAATTTTGGTTCCAAATATTTGACATGAAGAAGTGGGATCAGT 740

Qy        721 TTTACAGTGAAGTTTTAGGAAGACCCACTACCTTATTTGAGACAATGGGAAAAGCTGACA 780
              | |||||||||||  |||||||||||||||||| |||| |||||||||| ||||||||||
Db        741 TCTACAGTGAAGTTCTAGGAAGACCCACTACGTTATCTGAGACAATGGCAAAAGCTGACA 800

Qy        781 TATGGCTTATGCGAAACTCCTGGAGTTTTCAATTTCCTCATCCATTCTTACCAAACGTTG 840
              |||||||||| ||||||| ||||  |||||||||||||||| ||| |||||||||| ||||
Db        801 TATGGCTTATTCGAAACTACTGGGATTTTCAATTTCCTCACCCACTCTTACCAAATGTTG 860

Qy        841 ATTTTGTTGGAGGATTCCACTGGCAAACCTGCCAAACCCCTACCTAAGGAAATGGAGGAG 900
              | || ||||||||| |||||| |||||||||||||||||||||| |||||||||| |||
Db        861 AGTTCGTTGGAGGACTCCACT-GCAAACCTGCCAAACCCCTACCGAAGGAAATGGAAGAG 919

Qy        901 TTTGTACAGAGCTCTGGAGAAAATGGTGTTGTGGTGTTTTCTCTGGGGTCAGTGATAAGT 960
              ||||| |||||||||||||||||||||||||||||||||||||||||||  || | |||
Db        920 TTTGTCCAGAGCTCTGGAGAAAATGGTGTTGTGGTGTTTTCTCTGGGGTCGATGGTCAGT 979
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Qy        961 AACATGACAGCAGAAAGGGCCAATGTAATTGCAACAGCCCTTGCCAAGATCCCACAAAAG 1020
              |||| | ||| ||||||||||||||||||||||| |||||||||||||||||||||||||
Db        980 AACACGTCAGAAGAAAGGGCCAATGTAATTGCATCAGCCCTTGCCAAGATCCCACAAAAG 1039

Qy       1021 GTTCTGTGGAGATTTGATGGGAATAAACCAGATGCCTTAGGTCTCAATACTCGGCTGTAT 1080
              |||||||||||||||||||||||||||||||| | ||||| ||||||||||||||||||
Db       1040 GTTCTGTGGAGATTTGATGGGAATAAACCAGATACTTTAGGACTCAATACTCGGCTGTAC 1099

Qy       1081 AAGTGGATACCCCAGAATGACCTTCTAGGTCATCCAAAAACCAGAGCTTTTATAACTCAT 1140
              |||||||||||||||||||| ||||| ||||| ||||||||||||||||||||||||||||
Db       1100 AAGTGGATACCCCAGAATGATCTTCTTGGTCACCCAAAAACCAGAGCTTTTATAACTCAT 1159

Qy       1141 GGTGGAGCCAATGGCATCTATGAGGCAATCTACCATGGGATCCCTATGGTGGGCATTCCA 1200
              |||||||||||||||||||||||||||||||||||||| |||||||||||||| |||||
Db       1160 GGTGGAGCCAATGGCATCTATGAGGCAATCTACCATGGAATCCCTATGGTGGGCGTTCCA 1219

Qy       1201 TTGTTTTGGGATCAACCTGATAACATTGCTCACATGAAGGCCAAGGGAGCAGCTGTTAGA 1260
              ||||||   |||||||||||||||||||| ||||||||||||||||||||||||||||||
Db       1220 TTGTTTGCAGATCAACCTGATAACATTGCACACATGAAGGCCAAGGGAGCAGCTGTTAGT 1279

Qy       1261 TTGGACTTCAACACAATGTCGAGTACAGACCTGCTGAATGCACTGAAGACAGTAATTAAT 1320
              ||||||||| |||||||||||||||||||| | || ||||||||||||||||||||||||
Db       1280 TTGGACTTCCACACAATGTCGAGTACAGACTTACTCAATGCACTGAAGACAGTAATTAAT 1339

Qy       1321 GATCCTTTATATAAAGAGAATATTATGAAATTATCAAGAATTCAACATGATCAACCAGTA 1380
              |||||||||||||||||||  |||||||||||||||||||| ||||||||||||||
Db       1340 GATCCTTTATATAAAGAGAATGCTATGAAATTATCAAGAATTCATCATGATCAACCAGTG 1399

Qy       1381 AAGCCCCTGGATCGAGCAGTCTTCTGGATTGAATTTGTCATGCCCCACAAAGGAGCCAAA 1440
              |||||||| |||||||||||||||||||||||||||||||| ||| ||||||||||||
Db       1400 AAGCCCCTTGATCGAGCAGTCTTCTGGATTGAATTTGTCATGCGCCATAAAGGAGCCAAG 1459

Qy       1441 CACCTTCGAGTTGCAGCCCATGACCTCACCTGGTTCCAGTACCACTCTTTGGATGTGATT 1500
              |||||||| |||||||||||| |||||||||||||||||||||||||||||||||||| |
Db       1460 CACCTTCGGGTTGCAGCCCACGACCTCACCTGGTTCCAGTACCACTCTTTGGATGTGACT 1519

Qy       1501 GGGTTTCTGCTGGCCTGTGTGGCAACTGTGATATTTATCATCACAAAGTTTTGTCTGTTT 1560
              ||||| |||||||||||||||||||||||||||||| ||||||||||    |||||||||
Db       1520 GGGTTCCTGCTGGCCTGTGTGGCAACTGTGATATTCATCATCACAAA---ATGTCTGTTT 1576

Qy       1561 TGTTTCTGGAAGTTTGCTAGAAAAGGGAAGAAGGGAAAAAGAGATTAGTTATGTCTGACA 1620
              ||| |||||||||||| ||||| ||| |||||||| |||||||||| ||| ||||||
Db       1577 TGTGTCTGGAAGTTTGTTAGAACAGGAAAGAAGGGGAAAAGAGATTAATTACGTCTGAGG 1636

Qy       1621 TTTGAAGCTGGAAAACCAGATAGATAGGACAACTTCAGTTTATTCCAGCAAGAAAGAAAA 1680
               | |||||||| |||||  ||| || | ||  ||| |||||||| || ||||||   |
Db       1637 CTGGAAGCTGGGAAACCCAATAAAT-GAACTCCTTTAGTTTATTACAACAAGAA--GACG 1693

Qy       1681 GATTGTTATGCAAGATTTCTTTCTTCCTGTGAC 1713
                || ||    ||||| |||||||| ||||||
Db       1694 TTGTGATACAAGAGATTCCTTTCTTCTTGTGAC 1726
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Search completed: September 3, 2005, 12:14:13
Job time : 1172 secs

GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: September 3, 2005, 04:54:03 ; Search time 331 Seconds
(without alignments)
8468.103 Million cell updates/sec

Title: US-09-721-183-2
Perfect score: 1713
Sequence: 1 atcgcattgcaccaggatga.....gatttctttcttcctgtgac 1713

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_NA:*
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2: /cgn2_6/ptodata/1/ina/5B_COMB.seq:*
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6: /cgn2_6/ptodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1564.4	91.3	1708	4	US-09-949-016-2595	Sequence 2595, Ap
2	1519	88.7	1629	4	US-09-949-016-2596	Sequence 2596, Ap
3	1443.6	84.3	1854	4	US-09-356-806-39	Sequence 39, Appl
4	1364.2	79.6	1832	4	US-09-949-016-2734	Sequence 2734, Ap
5	1354.2	79.1	2092	4	US-09-356-806-7	Sequence 7, Appli
6	1349.4	78.8	2092	4	US-09-949-016-2594	Sequence 2594, Ap
7	1349.4	78.8	2092	4	US-09-949-016-3181	Sequence 3181, Ap
8	1343	78.4	2093	4	US-09-949-016-1128	Sequence 1128, Ap
9	1201.6	70.1	2107	3	US-09-180-852-1	Sequence 1, Appli
10	1188.8	69.4	1976	4	US-09-356-806-112	Sequence 112, App
11	1128.8	65.9	1413	3	US-09-813-918-1	Sequence 1, Appli
12	1128.8	65.9	1413	4	US-10-060-311-1	Sequence 1, Appli
13	941.8	55.0	1323	4	US-09-949-016-2735	Sequence 2735, Ap
14	941.8	55.0	1323	4	US-09-949-016-2736	Sequence 2736, Ap
15	742.8	43.4	2966	4	US-09-976-594-241	Sequence 241, App
16	674.6	39.4	18373	4	US-09-949-016-14338	Sequence 14338, A
17	674.6	39.4	18452	4	US-09-949-016-14337	Sequence 14337, A
18	634.6	37.0	1001	4	US-09-671-317-403	Sequence 403, App
19	602.6	35.2	1686	4	US-09-356-806-41	Sequence 41, Appl
20	579.2	33.8	1323	4	US-09-356-806-1	Sequence 1, Appli
21	579.2	33.8	19732	4	US-09-949-016-12870	Sequence 12870, A
22	579.2	33.8	19732	4	US-09-949-016-14923	Sequence 14923, A
23	579.2	33.8	19733	4	US-09-949-016-14336	Sequence 14336, A
24	520	30.4	20441	4	US-09-949-016-14476	Sequence 14476, A
25	491.4	28.7	2312	4	US-09-356-806-114	Sequence 114, App
26	489.8	28.6	20599	4	US-09-949-016-14477	Sequence 14477, A
27	489.8	28.6	20599	4	US-09-949-016-14478	Sequence 14478, A
28	480.4	28.0	1001	4	US-09-671-317-412	Sequence 412, App
29	326.6	19.1	596	4	US-09-356-806-45	Sequence 45, Appl
30	320	18.7	1001	4	US-09-671-317-405	Sequence 405, App
31	319.4	18.6	2339	5	PCT-US92-00282-2	Sequence 2, Appli
32	299.6	17.5	2351	4	US-09-949-016-76	Sequence 76, Appl
33	299.6	17.5	2351	4	US-09-949-016-1813	Sequence 1813, Ap
34	298	17.4	2336	5	PCT-US92-00282-1	Sequence 1, Appli
35	266.2	15.5	1589	4	US-09-356-806-6	Sequence 6, Appli
36	265.8	15.5	735	4	US-09-305-856B-17	Sequence 17, Appl
37	264.2	15.4	1001	4	US-09-671-317-352	Sequence 352, App
38	263	15.4	1001	4	US-09-671-317-353	Sequence 353, App
39	263	15.4	1001	4	US-09-671-317-354	Sequence 354, App
40	246	14.4	978	4	US-09-356-806-118	Sequence 118, App
41	244.4	14.3	1001	4	US-09-671-317-427	Sequence 427, App
42	230	13.4	1001	4	US-09-671-317-424	Sequence 424, App
43	220.6	12.9	350	4	US-09-513-999C-3284	Sequence 3284, Ap
44	217	12.7	1001	4	US-09-671-317-428	Sequence 428, App
45	208.4	12.2	1001	4	US-09-671-317-404	Sequence 404, App

ALIGNMENTS

RESULT 1
US-09-949-016-2595
; Sequence 2595, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2595
; LENGTH: 1708
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-2595

Query Match 91.3%; Score 1564.4; DB 4; Length 1708;
Best Local Similarity 96.0%; Pred. No. 0;
Matches 1638; Conservative 0; Mismatches 61; Indels 7; Gaps 3;

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Qy          8 TGCACCAGGATGACTCTGAAATGGACTTCAGTTCTTCTGCTGATACATCTCCAGTTGTTA 67
              ||||||||||||  |||||||||| |||||||||||||||||||||||| |||||||||
Db          1 TGCACCAGGATGGTTCTGAAATGGGCTTCAGTTCTTCTGCTGATACATCT-CAGTTGTTA 59

Qy         68 CTTTAGCTCTGGGAGTTGTGGAAAAGTGCTGGTGTGGGCCGCAGAATACAGCCATTGGAT 127
              ||||||||||||||||||||||| |||||||| |||||| |||||||||||| ||||||
Db         60 CTTTAGCTCTGGGAGTTGTGGAAAGGTGCTGGTTTGGGCCACAGAATACAGCCTTTGGAT 119

Qy        128 GAATATGAAGACAATCCTGAAAGAGCTTGTTCAGAGAGGTCATGAGGTGACTGTACTGGC 187
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        120 GAATATGAAGACAATCCTGAAAGAGCTTGTTCAGAGAGGTCATGAGGTGACTGTACTGGC 179

Qy        188 ATCTTCAGCTTCCATTCTTTTTGATCCCAATGATGCATCCACTCTTAAATTTGAAGTTTA 247
              |||||||||||||||||||||||||||||| ||  |||||||||||||| | ||||||||
Db        180 ATCTTCAGCTTCCATTCTTTTTGATCCCAACGACTCATCCACTCTTAAACTCGAAGTTTA 239

Qy        248 TCCTACATCTTTAACTAAAACTGAATTTGAGAATATCATCATGCAACAGGTTAAGAGATG 307
              ||||||||||||||||||||||||||||||||||||| ||||||||||||||||||||||
Db        240 TCCTACATCTTTAACTAAAACTGAATTTGAGAATATCGTCATGCAACAGGTTAAGAGATG 299

Qy        308 GTCAGACATTCGAAAAGATAGCTTTTGGTTATATTTTTCACAAGAACAAGAAATCCTGTG 367
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Db        300 GTCAGACATTCCAAAAGATACATTTTGGTTATATTTTTCACAAGAACAAGAAATGCTGTA 359

Qy        368 GGAATTATATGACATATTTAGAAACTTCTGTAAAGATGTAGTTTCAAATAAGAAAGTTAT 427

Db        360 GGAATTACATGACATATTTAGAAAATTCTGTAAAGATCTCATTTCAAATAAGAAACTTAT 419

Qy        428 GAAAAAACTACAAGAGTCAAGATTTGACATCGTTTTTGCAGATGCTGTTTTTCCCTGTGG 487

Db        420 GAAAAAACTATAAGAGTCAAGATTTGACATCGTTTTTGCAGATGCTTTTTTTCCCTGTGG 479

Qy        488 TGAGCTGCTGGCTGCGCTACTTAACATACGGTTTGTGTACAGTCTCCGCTTTACTCCTGG 547

Db        480 TGAGCTGCTGGCTGCGCTACTTAACATACCCTTTGTGTACAGTCTCCGCTTTACTCCTGG 539

Qy        548 CTACACAATTGAAAGGCACAGTGGAGGACTGATTTTCCCTCCTTCCTACATACCTATTGT 607

Db        540 CTACACAGTTGAAAGGCACAGTGGAGGACTGATTTTCCCTCCTTCCTACATACCTATTGT 599

Qy        608 TATGTCAAAATTAAGTGATCAAATGACTTTCATGGAGAGGGTAAAAAATATGATCTATGT 667

Db        600 TATGTCAAAATTAAGTGATCAAATGACTTTCATGGAGAGGGTAAAAAATATGATCTATGT 659

Qy        668 GCTTTATTTTGACTTTTGGTTCCAAATGTCTGATATGAAGAAGTGGGATCAGTTTTACAG 727

Db        660 GATTTATTTTGACTTTTGGTTCCAAATATGTGATATGAAGAAGTGGGATCAGTTTTACAG 719

Qy        728 TGAAGTTTTAGGAAGACCCACTACCTTATTTGAGACAATGGGAAAAGCTGACATATGGCT 787

Db        720 TGAAGTTTTAGGAAGACCCACTACCTTATTTGAGACAATGGGGAAAGCTGACATATGGCT 779

Qy        788 TATGCGAAACTCCTGGAGTTTTCAATTTCCTCATCCATTCTTACCAAACGTTGATTTTGT 847

Db        780 TATGCGAAACTCCTGGAATTTTCAGTTTCCTCATCCATTCTTACCAAACGTTGATTTTGT 839

Qy        848 TGGAGGATTCCACTGGCAAACCTGCCAAACCCCTACCTAAGGAAATGGAGGAGTTTGTAC 907

Db        840 TGGAGGATTTCACT-GCAAACCTGCCAAACCCCTACCTAAGGAAATGGAGGAGTTTGTAC 898

Qy        908 AGAGCTCTGGAGAAAATGGTGTTGTGGTGTTTTCTCTGGGGTCAGTGATAAGTAACATGA 967

Db        899 AGAGCTCTGGAGAAAATGGTGTTGTGGTGTTTTCTCTGGGGTCAATGGTCAGTAACATGA 958

Qy        968 CAGCAGAAAGGGCCAATGTAATTGCAACAGCCCTTGCCAAGATCCCACAAAAGGTTCTGT 1027

Db        959 CAGCAGAAAGGGCCAACGTAATTGCAACAGCCCTTGCCAAGATCCCACAAAAGGTTCTGT 1018

Qy       1028 GGAGATTTGATGGGAATAAACCAGATGCCTTAGGTCTCAATACTCGGCTGTATAAGTGGA 1087

Db       1019 GGAGATTTGATGGGAATAAACCAGATGCTTTAGGTCTCAATACTCGGCTGTACAAGTGGA 1078

Qy       1088 TACCCCAGAATGACCTTCTAGGTCATCCAAAAACCAGAGCTTTTATAACTCATGGTGGAG 1147

Db       1079 TACCCCAGAATGACCTTCTAGGTCATCCAAAAACCAGAGCTTTTATAACTCATGGTGGAG 1138

Qy       1148 CCAATGGCATCTATGAGGCAATCTACCATGGGATCCCTATGGTGGGCATTCCATTGTTTT 1207

Db       1139 CAAGTGGCATCTATGAGGCAATCTACCATGGGATCCCTATGGTGGGCATTCCATTGTTTT 1198

Qy       1208 GGGATCAACCTGATAACATTGCTCACATGAAGGCCAAGGGAGCAGCTGTTAGATTGGACT 1267

Db       1199 GGGATCAACCTGATAACATTGCTCACATGAAGGCCAAGGGAGCAGCTGTTAGACTGGACT 1258

Qy       1268 TCAACACAATGTCGAGTACAGACCTGCTGAATGCACTGAAGACAGTAATTAATGATCCTT 1327

Db       1259 TCCACACAATGTCGAGTACAGACCTGCTGAATGCACTGAAGACAGTAATTAATGATCCTT 1318

Qy       1328 TATATAAAGAGAATATTATGAAATTATCAAGAATTCAACATGATCAACCAGTAAAGCCCC 1387

Db       1319 TATATAAAGAGAATATTATGAAATTATCAAGAATTCAACATGATCAACCAGTAAAGCCCC 1378

Qy       1388 TGGATCGAGCAGTCTTCTGGATTGAATTTGTCATGCCCCACAAAGGAGCCAAACACCTTC 1447

Db       1379 TGGATCGAGCAGTCTTCTGGATTGAATTTGTCATGCGCCACAAAGGAGCCAAACACCTTC 1438

Qy       1448 GAGTTGCAGCCCATGACCTCACCTGGTTCCAGTACCACTCTTTGGATGTGATTGGGTTTC 1507

Db       1439 GAGTTGCAGCCCGTGACCTCACCTGGTTCCAGTACCACTCTTTGGATGTGATTGGGTTTC 1498

Qy       1508 TGCTGGCCTGTGTGGCAACTGTGATATTTATCATCACAAAGTTTTGTCTGTTTTGTTTCT 1567

Db       1499 TGCTGGCCTGTGTGGCAACTGTGACATTTATCATCACAAAGTGTTGTCTGTTTTGTTTCT 1558

Qy       1568 GGAAGTTTGCTAGAAAAGGGAAGAAGGGAAAAAGAGATTAGTTATGTCTGACATTTGAAG 1627

Db       1559 GGAAGTTTACTAGAAAAGTGAAGAAGGAAAAAAGGGATTAGTTATGTCCGACATTTGAAG 1618

Qy       1628 CTGGAAAACCAGATAGATAGGACAACTTCAGTTTATTCCAGCAAGAAAGAAAAGATTGTT 1687

Db       1619 CTGGAAAACCTGATAGATGGGATGACTTCAGTTTATTCCAGCAAG-----AAAGATTGTG 1673

Qy       1688 ATGCAAGATTTCTTTCTTCCTGTGAC 1713

Db       1674 ATGCAAGATTTCTTTCTTCCTATGAC 1699


RESULT 2
US-09-949-016-2596
; Sequence 2596, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
;  APPLICANT: VENTER, J. Craig et al.
;  TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
;  TITLE OF INVENTION:  WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001307
;  CURRENT APPLICATION NUMBER: US/09/949,016
;  CURRENT FILING DATE:  2000-04-14
;  PRIOR APPLICATION NUMBER: 60/241,755
;  PRIOR FILING DATE: 2000-10-20
;  PRIOR APPLICATION NUMBER: 60/237,768
;  PRIOR FILING DATE: 2000-10-03
;  PRIOR APPLICATION NUMBER: 60/231,498
;  PRIOR FILING DATE: 2000-09-08
;  NUMBER OF SEQ ID NOS: 207012
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2596
;   LENGTH: 1629
;   TYPE: DNA
;   ORGANISM: Human
US-09-949-016-2596

  Query Match            88.7%;  Score 1519;  DB 4;  Length 1629;
  Best Local Similarity  96.5%;  Pred. No. 0;
  Matches 1574;  Conservative    0;  Mismatches   55;  Indels    2;  Gaps    2;

Qy          7 TTGCACCAGGATGACTCTGAAATGGACTTCAGTTCTTCTGCTGATACATCTCCAGTTGTT 66

Db          1 TTGCACCAGGATGGTTCTGAAATGGGCTTCAGTTCTTCTGCTGATACATCT-CAGTTGTT 59

Qy         67 ACTTTAGCTCTGGGAGTTGTGGAAAAGTGCTGGTGTGGGCCGCAGAATACAGCCATTGGA 126

Db         60 ACTTTAGCTCTGGGAGTTGTGGAAAGGTGCTGGTTTGGGCCACAGAATACAGCCTTTGGA 119

Qy        127 TGAATATGAAGACAATCCTGAAAGAGCTTGTTCAGAGAGGTCATGAGGTGACTGTACTGG 186

Db        120 TGAATATGAAGACAATCCTGAAAGAGCTTGTTCAGAGAGGTCATGAGGTGACTGTACTGG 179

Qy        187 CATCTTCAGCTTCCATTCTTTTTGATCCCAATGATGCATCCACTCTTAAATTTGAAGTTT 246

Db        180 CATCTTCAGCTTCCATTCTTTTTGATCCCAACGACTCATCCACTCTTAAACTCGAAGTTT 239

Qy        247 ATCCTACATCTTTAACTAAAACTGAATTTGAGAATATCATCATGCAACAGGTTAAGAGAT 306

Db        240 ATCCTACATCTTTAACTAAAACTGAATTTGAGAATATCGTCATGCAACAGGTTAAGAGAT 299

Qy        307 GGTCAGACATTCGAAAAGATAGCTTTTGGTTATATTTTTCACAAGAACAAGAAATCCTGT 366
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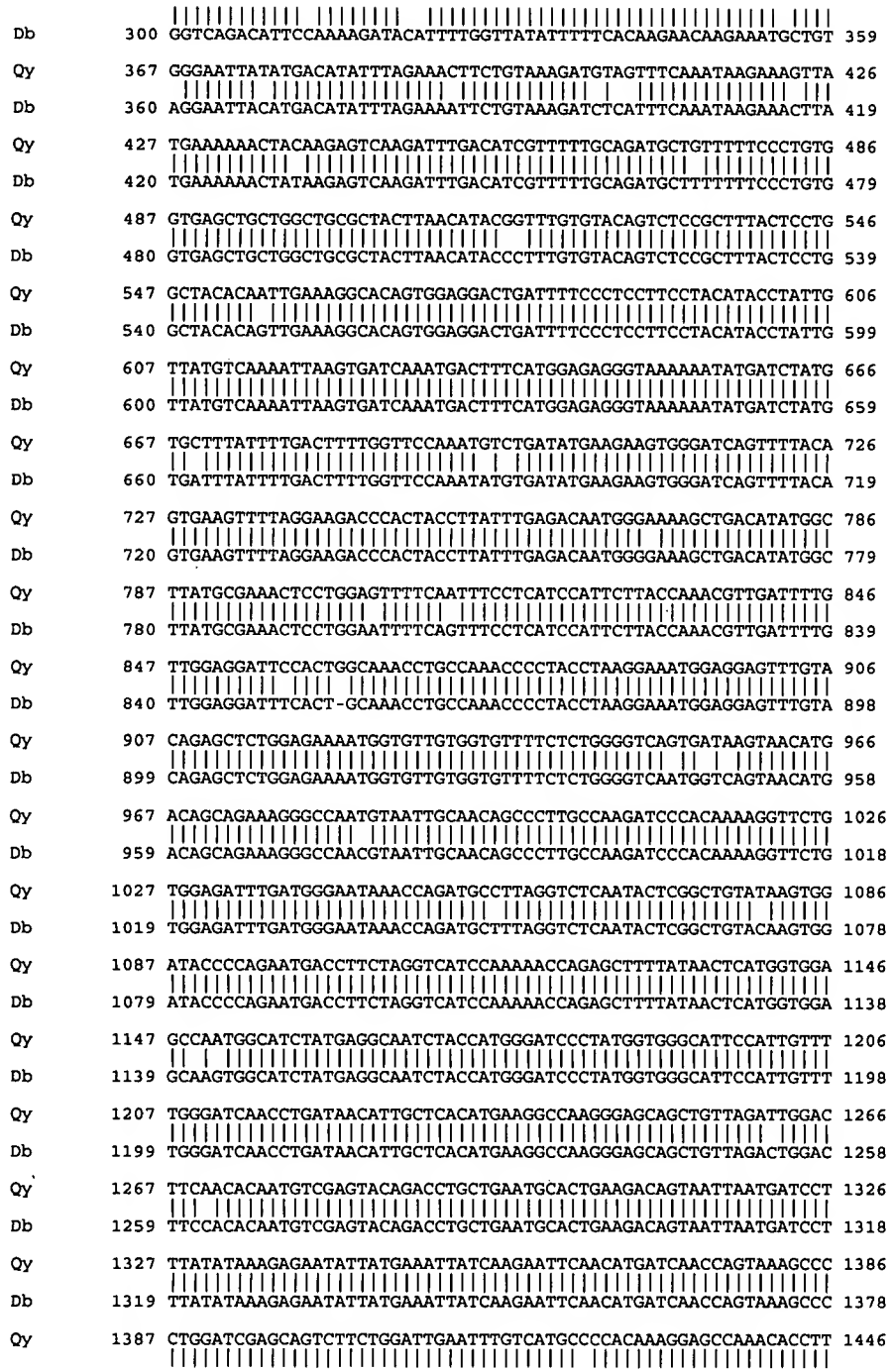

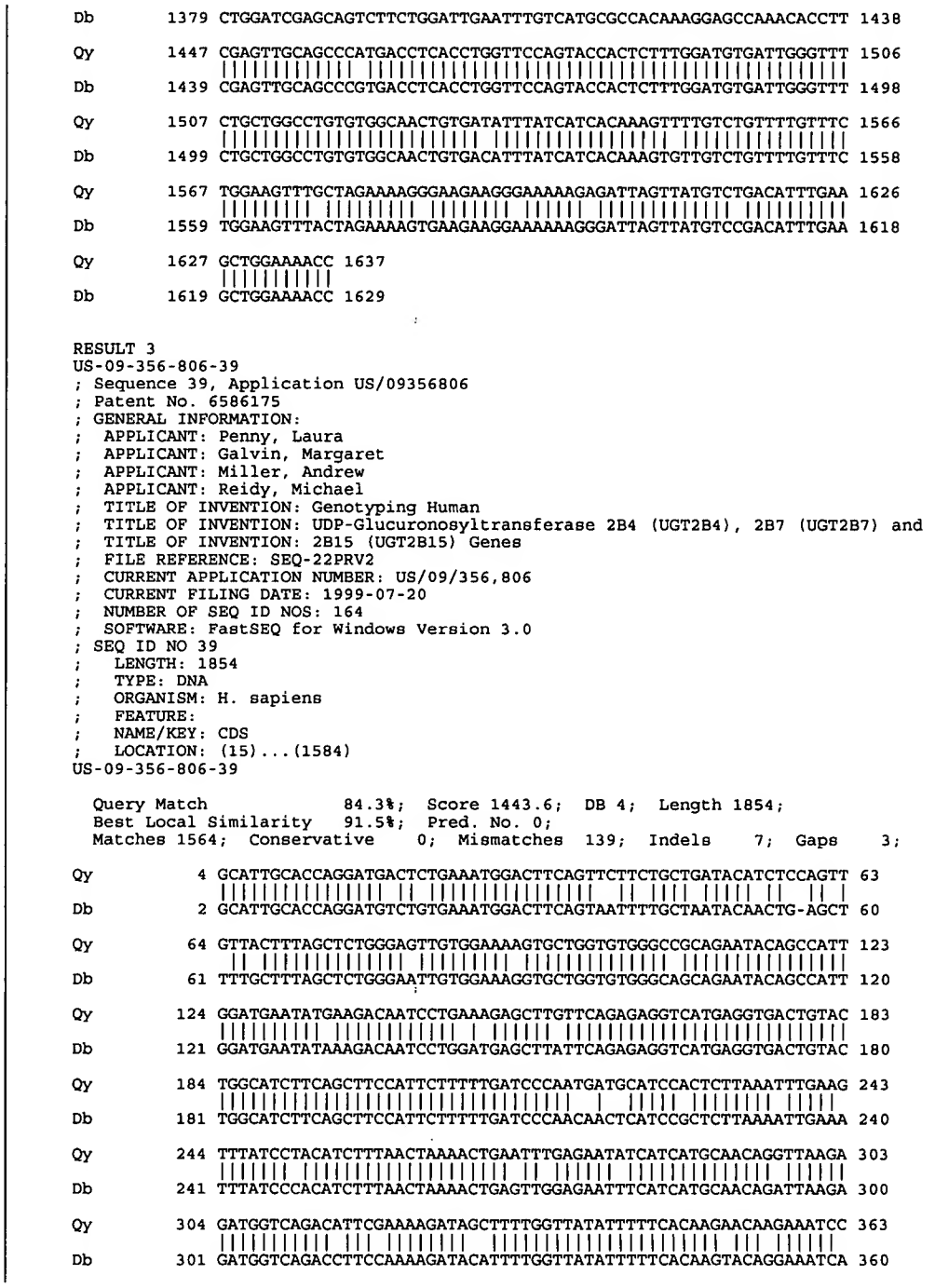

RESULT 3
US-09-356-806-39
; Sequence 39, Application US/09356806
; Patent No. 6586175
; GENERAL INFORMATION:
; APPLICANT: Penny, Laura
; APPLICANT: Galvin, Margaret
; APPLICANT: Miller, Andrew
; APPLICANT: Reidy, Michael
; TITLE OF INVENTION: Genotyping Human
; TITLE OF INVENTION: UDP-Glucuronosyltransferase 2B4 (UGT2B4), 2B7 (UGT2B7) and
; TITLE OF INVENTION: 2B15 (UGT2B15) Genes
; FILE REFERENCE: SEQ-22PRV2
; CURRENT APPLICATION NUMBER: US/09/356,806
; CURRENT FILING DATE: 1999-07-20
; NUMBER OF SEQ ID NOS: 164
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 39
; LENGTH: 1854
; TYPE: DNA
; ORGANISM: H. sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (15)...(1584)
US-09-356-806-39

Query Match 84.3%; Score 1443.6; DB 4; Length 1854;
Best Local Similarity 91.5%; Pred. No. 0;
Matches 1564; Conservative 0; Mismatches 139; Indels 7; Gaps 3;

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Qy       364 TGTGGGAATTATATGACATATTTAGAAACTTCTGTAAAGATGTAGTTTCAAATAAGAAAG 423
Db       361 TGTCAATATTTGGTGACATAACTAGAAAGTTCTGTAAAGATGTAGTTTCAAATAAGAAAT 420

Qy       424 TTATGAAAAAACTACAAGAGTCAAGATTTGACATCGTTTTTGCAGATGCTGTTTTTCCCCT 483
Db       421 TTATGAAAAAAGTACAAGAGTCAAGATTTGACGTCATTTTTGCAGATGCTATTTTTCCCT 480

Qy       484 GTGGTGAGCTGCTGGCTGCGCTACTTAACATACGGTTTGTGTACAGTCTCCGCTTTACTC 543
Db       481 GTAGTGAGCTGCTGGCTGAGCTATTTAACATACCCTTTGTGTACAGTCTCAGCTTCTCTC 540

Qy       544 CTGGCTACACAATTGAAAGGCACAGTGGAGGACTGATTTTCCCTCCTTCCTACATACCTA 603
Db       541 CTGGCTACACTTTTGAAAAGCATAGTGGAGGATTTATTTTCCCTCCTTCCTACGTACCTG 600

Qy       604 TTGTTATGTCAAAATTAAGTGATCAAATGACTTTCATGGAGAGGGTAAAAAATATGATCT 663
Db       601 TTGTTATGTCAGAATTAACTGATCAAATGACTTTCATGGAGAGGGTAAAAAATATGATCT 660

Qy       664 ATGTGCTTTATTTTGACTTTTGGTTCCAAATGTCTGATATGAAGAAGTGGGATCAGTTTT 723
Db       661 ATGTGCTTTACTTTGACTTTTGGTTCGAAATATTTGACATGAAGAAGTGGGATCAGTTTT 720

Qy       724 ACAGTGAAGTTTTAGGAAGACCCACTACCTTATTTGAGACAATGGGAAAAGCTGACATAT 783
Db       721 ATAGTGAAGTTCTAGGAAGACCCACTACATTATCTGAGACAATGGGGAAAGCTGACGTAT 780

Qy       784 GGCTTATGCGAAACTCCTGGAGTTTTCAATTTCCTCATCCATTCTTACCAAACGTTGATT 843
Db       781 GGCTTATTCGAAACTCCTGGAATTTTCAGTTTCCATATCCACTCTTACCAAATGTTGATT 840

Qy       844 TTGTTGGAGGATTCCACTGGCAAACCTGCCAAACCCCTACCTAAGGAAATGGAGGAGTTT 903
Db       841 TTGTTGGAGGACTCCACT-GCAAACCTGCCAAACCCCTGCCTAAGGAAATGGAAGACTTT 899

Qy       904 GTACAGAGCTCTGGAGAAAATGGTGTTGTGGTGTTTTCTCTGGGGTCAGTGATAAGTAAC 963
Db       900 GTACAGAGCTCTGGAGAAAATGGTGTTGTGGTGTTTTCTCTGGGGTCAATGGTCAGTAAC 959

Qy       964 ATGACAGCAGAAAGGGCCAATGTAATTGCAACAGCCCTTGCCAAGATCCCACAAAAGGTT 1023
Db       960 ATGACAGAAGAAAGGGCCAACGTAATTGCATCAGCCCTGGCCCAGATCCCACAAAAGGTT 1019

Qy      1024 CTGTGGAGATTTGATGGGAATAAACCAGATGCCTTAGGTCTCAATACTCGGCTGTATAAG 1083
Db      1020 CTGTGGAGATTTGATGGGAATAAACCAGATACCTTAGGTCTCAATACTCGGCTCTACAAG 1079

Qy      1084 TGGATACCCCAGAATGACCTTCTAGGTCATCCAAAAACCAGAGCTTTTATAACTCATGGT 1143
Db      1080 TGGATACCCCAGAATGACCTTCTAGGTCATCCAAAGACCAGAGCTTTTATAACTCATGGT 1139

Qy      1144 GGAGCCAATGGCATCTATGAGGCAATCTACCATGGGATCCCTATGGTGGGCATTCCATTG 1203
Db      1140 GGAGCCAATGGCATCTACGAGGCAATCTACCATGGGATCCCTATGGTGGGGATTCCATTG 1199

Qy      1204 TTTTGGGATCAACCTGATAACATTGCTCACATGAAGGCCAAGGGAGCAGCTGTTAGATTG 1263
Db      1200 TTTGCCGATCAACCTGATAACATTGCTCACATGAAGGCCAGGGGAGCAGCTGTTAGAGTG 1259

Qy      1264 GACTTCAACACAATGTCGAGTACAGACCTGCTGAATGCACTGAAGACAGTAATTAATGAT 1323
Db      1260 GACTTCAACACAATGTCGAGTACAGACTTGCTGAATGCATTGAAGAGAGTAATTAATGAT 1319

Qy      1324 CCTTTATATAAAGAGAATATTATGAAATTATCAAGAATTCAACATGATCAACCAGTAAAG 1383
Db      1320 CCTTCATATAAAGAGAATGTTATGAAATTATCAAGAATTCAACATGATCAACCAGTGAAG 1379

Qy      1384 CCCCTGGATCGAGCAGTCTTCTGGATTGAATTTGTCATGCCCCACAAAGGAGCCAAACAC 1443
Db      1380 CCCCTGGATCGAGCAGTCTTCTGGATTGAATTTGTCATGCGCCACAAAGGAGCTAAACAC 1439

Qy      1444 CTTCGAGTTGCAGCCCATGACCTCACCTGGTTCCAGTACCACTCTTTGGATGTGATTGGG 1503
Db      1440 CTTCGGGTTGCAGCCCACGACCTCACCTGGTTCCAGTACCACTCTTTGGATGTGATTGGG 1499

Qy      1504 TTTCTGCTGGCCTGTGTGGCAACTGTGATATTTATCATCACAAAGTTTTGTCTGTTTTGT 1563
Db      1500 TTCCTGCTGGTCTGTGTGGCAACTGTGATATTTATCGTCACAAAATGTTGTCTGTTTTGT 1559

Qy      1564 TTCTGGAAGTTTGCTAGAAAAGGGAAGAAGGGAAAAAGAGATTAGTTATGTCTGACATTT 1623
Db      1560 TTCTGGAAGTTTGCTAGAAAAGCAAAGAAGGGAAAAAATGATTAGTTATATCTGAGATTT 1619

Qy      1624 GAAGCTGGAAAACCAGATAGATAGGACAACTTCAGTTTATTCCAGCAAGAAAGAAAAGAT 1683
Db      1620 GAAGCTGGAAAACCTGATAGGTGAGACTACTTCAGTTTATTCCAGCAAG-----AAAGAT 1674

Qy      1684 TGTTATGCAAGATTTCTTTCTTCCTGTGAC 1713
Db      1675 TGTGATGCAAGATTTCTTTCTTCCTGAGAC 1704
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RESULT 4
US-09-949-016-2734
; Sequence 2734, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2734
; LENGTH: 1832
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(1832)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-2734

Query Match 79.6%; Score 1364.2; DB 4; Length 1832;
Best Local Similarity 89.2%; Pred. No. 0;
Matches 1526; Conservative 0; Mismatches 153; Indels 32; Gaps 5;

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Db         2 GCATTGCACCAGGATGTCTGTGAAATGGACTTCAGTAATTTTGCTAATACAACTG-AGCT 60

Qy        64 GTTACTTTAGCTCTGGGAGTTGTGGAAAAGTGCTGGTGTGGGCCGCAGAATACAGCCATT 123
Db        61 TTTGCTTTAGCTCTGGGAATTGTGGAAAGGTGCTGGTGTGGGCAGCAGAATACAGCCATT 120

Qy       124 GGATGAATATGAAGACAATCCTGAAAGAGCTTGTTCAGAGAGGTCATGAGGTGACTGTAC 183
Db       121 GGATGAATATAAAGACAATCCTGGATGAGCTTATTCAGAGAGGTCATGAGGTGACTGTAC 180

Qy       184 TGGCATCTTCAGCTTCCATTCTTTTTGATCCCAATGATGCATCCACTCTTAAATTTGAAG 243
Db       181 TGGCATCTTCAGCTTCCATTCTTTTTGATCCCAACAACTCATCCGCTCTTAAAATTGAAA 240

Qy       244 TTTATCCTACATCTTTAACTAAAACTGAATTTGAGAATATCATCATGCAACAGGTTAAGA 303
Db       241 TTTATCCCACATCTTTA----------NNNNNNNNNNNNNNNNNN 276
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Qy        304 GATGGTCAGACATTCGAAAAGATAGCTTTTGGTTATATTTTTCACAAGAACA-AGAAATC 362
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Db        277 NNTGGTCAGACCTTCCAAAAGATACATTTTGGTTATATTTTTCACAAGTACAGGGAAATC 336

Qy        363 CTGTGGGAATTATATGACATATTTAGAAACTTCTGTAAAGATGTAGTTTCAAATAAGAAA 422
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Db        337 ATGTCAATATTTGGTGACATAACTAGAAAGTTCTGTAAAGATGTAGTTTCAAATAAGAAA 396

Qy        423 GTTATGAAAAAACTACAAGAGTCAAGATTTGACATCGTTTTTGCAGATGCTGTTTTTCCC 482
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Db        397 TTTATGAAAAAAGTACAAGAGTCAAGATTTGACGTCATTTTTGCAGATGCTATTTTTCCC 456

Qy        483 TGTGGTGAGCTGCTGGCTGCGCTACTTAACATACGGTTTGTGTACAGTCTCCGCTTTACT 542
              ||| ||||||||||||||| |||| |||||||||  ||||||||||||||| |||| ||
Db        457 TGTAGTGAGCTGCTGGCTGAGCTATTTAACATACCCTTTGTGTACAGTCTCAGCTTCTCT 516

Qy        543 CCTGGCTACACAATTGAAAGGCACAGTGGAGGACTGATTTTCCCTCCTTCCTACATACCT 602
              |||||||||| |||||| ||| ||||||||| | ||||||||||||||||||| |||||
Db        517 CCTGGCTACACTTTTGAAAAGCATAGTGGAGGATTTATTTTCCCTCCTTCCTACGTACCT 576

Qy        603 ATTGTTATGTCAAAATTAAGTGATCAAATGACTTTCATGGAGAGGGTAAAAAATATGATC 662
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Db        577 GTTGTTATGTCAGAATTAACTGATCAAATGACTTTCATGGAGAGGGTAAAAAATATGATC 636

Qy        663 TATGTGCTTTATTTTGACTTTTGGTTCCAAATGTCTGATATGAAGAAGTGGGATCAGTTT 722
              |||||||||| |||||||||||||| |||| | ||| ||||||||||||||||||||||
Db        637 TATGTGCTTTACTTTGACTTTTGGTTCGAAATATTTGACATGAAGAAGTGGGATCAGTTT 696

Qy        723 TACAGTGAAGTTTTAGGAAGACCCACTACCTTATTTGAGACAATGGGAAAAGCTGACATA 782
              || ||||||||| |||||||||||||||| |||| |||||||||||| ||||||||| ||
Db        697 TATAGTGAAGTTCTAGGAAGACCCACTACATTATCTGAGACAATGGGGAAAGCTGACGTA 756

Qy        783 TGGCTTATGCGAAACTCCTGGAGTTTTCAATTTCCTCATCCATTCTTACCAAACGTTGAT 842
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Db        757 TGGCTTATTCGAAACTCCTGGAATTTTCAGTTTCCATATCCACTCTTACCAAATGTTGAT 816

Qy        843 TTTGTTGGAGGATTCCACTGGCAAACCTGCCAAACCCCTACCTAAGGAAATGGAGGAGTT 902
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Db        817 TTTGTTGGAGGACTCCACT-GCAAACCTGCCAAACCCCTGCCTAAGGAAATGGAAGACTT 875

Qy        903 TGTACAGAGCTCTGGAGAAAATGGTGTTGTGGTGTTTTCTCTGGGGTCAGTGATAAGTAA 962
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Db        876 TGTACAGAGCTCTGGAGAAAATGGTGTTGTGGTGTTTTCTCTGGGGTCAATGGTCAGTAA 935

Qy        963 CATGACAGCAGAAAGGGCCAATGTAATTGCAACAGCCCTTGCCAAGATCCCACAAAAGGT 1022
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Db        936 CATGACAGAAGAAAGGGCCAACGTAATTGCATCAGCCCTGGCCCAGATCCCACAAAAGGT 995

Qy       1023 TCTGTGGAGATTTGATGGGAATAAACCAGATGCCTTAGGTCTCAATACTCGGCTGTATAA 1082
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Db        996 TCTGTGGAGATTTGATGGGAATAAACCAGATACCTTAGGTCTCAATACTCGGCTGTATAA 1055

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Db       1056 GTGGATACCCCAGAATGACCTTCTAGGTCATCCAAAGACCAGAGCTTTTATAACTCATGG 1115

Qy       1143 TGGAGCCAATGGCATCTATGAGGCAATCTACCATGGGATCCCTATGGTGGGCATTCCATT 1202
              |||||||||||||||||| |||||||||||||||||||||||||||||| ||||||||
Db       1116 TGGAGCCAATGGCATCTACGAGGCAATCTACCATGGGATCCCTATGGTGGGGATTCCATT 1175

Qy       1203 GTTTTGGGATCAACCTGATAACATTGCTCACATGAAGGCCAAGGGAGCAGCTGTTAGATT 1262
              ||||  |||||||||||||||||||||||||||||||||||||||||||||||||||| |
Db       1176 GTTTGCCGATCAACCTGATAACATTGCTCACATGAAGGCCAGGGGAGCAGCTGTTAGAGT 1235

Qy       1263 GGACTTCAACACAATGTCGAGTACAGACCTGCTGAATGCACTGAAGACAGTAATTAATGA 1322
              |||||||||||||||||||||||||||||| |||||||||| |||||| ||||||||||
Db       1236 GGACTTCAACACAATGTCGAGTACAGACTTGCTGAATGCATTGAAGAGAGTAATTAATGA 1295

Qy       1323 TCCTTTATATAAAGAGAATATTATGAAATTATCAAGAATTCAACATGATCAACCAGTAAA 1382
              ||||| |||||||||||| ||||||||||||||||||||||||||||||||||||||||
Db       1296 TCCTTCATATAAAGAGAATGTTATGAAATTATCAAGAATTCAACATGATCAACCAGTGAA 1355

Qy       1383 GCCCCTGGATCGAGCAGTCTTCTGGATTGAATTTGTCATGCCCCACAAAGGAGCCAAACA 1442
              |||||||||||||||||||||||||||||||||||||||||||||| |||||||||| |||||
Db       1356 GCCCCTGGATCGAGCAGTCTTCTGGATTGAATTTGTCATGCGCCACAAAGGAGCTAAACA 1415

Qy       1443 CCTTCGAGTTGCAGCCCATGACCTCACCTGGTTCCAGTACCACTCTTTGGATGTGATTGG 1502
              |||||| |||||||||| ||||||||||||||||||||||||||||||||||||||||
Db       1416 CCTTCGGGTTGCAGCCCACGACCTCACCTGGTTCCAGTACCACTCTTTGGATGTGATTGG 1475

Qy       1503 GTTTCTGCTGGCCTGTGTGGCAACTGTGATATTTATCATCACAAAGTTTTGTCTGTTTTG 1562
              ||| ||||||| |||||||||||||||||||||||||||| ||||||| | ||||||||||||
Db       1476 GTTCCTGCTGGTCTGTGTGGCAACTGTGATATTTATCGTCACAAAATGTTGTCTGTTTTG 1535

Qy       1563 TTTCTGGAAGTTTGCTAGAAAAGGGAAGAAGGGAAAAAGAGATTAGTTATGTCTGACATT 1622
              |||||||||||||||||||||||  |||||||||||||  |||||||||| ||||| |||
Db       1536 TTTCTGGAAGTTTGCTAGAAAAGCAAAGAAGGGAAAAAATGATTAGTTATATCTGAGATT 1595

Qy       1623 TGAAGCTGGAAAACCAGATAGATAGGACAACTTCAGTTTATTCCAGCAAGAAAGAAAAGA 1682
              |||||||||||||||  ||||| |  ||| |||||||||||||||||||     |||||
Db       1596 TGAAGCTGGAAAACCTGATAGGTGAGACTACTTCAGTTTATTCCAGCAAG-----AAAGA 1650

Qy       1683 TTGTTATGCAAGATTTCTTTCTTCCTGTGAC 1713
              |||| |||||||||||||||||||| |||
Db       1651 TTGTGATGCAAGATTTCTTTCTTCCTGAGAC 1681


RESULT 5
US-09-356-806-7
; Sequence 7, Application US/09356806
; Patent No. 6586175
; GENERAL INFORMATION:
;  APPLICANT: Penny, Laura
;  APPLICANT: Galvin, Margaret
;  APPLICANT: Miller, Andrew
;  APPLICANT: Reidy, Michael
;  TITLE OF INVENTION: Genotyping Human
;  TITLE OF INVENTION: UDP-Glucuronosyltransferase 2B4 (UGT2B4), 2B7 (UGT2B7) and
;  TITLE OF INVENTION: 2B15 (UGT2B15) Genes
;  FILE REFERENCE: SEQ-22PRV2
;  CURRENT APPLICATION NUMBER: US/09/356,806
;  CURRENT FILING DATE: 1999-07-20
;  NUMBER OF SEQ ID NOS: 164
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 7
;   LENGTH: 2092
;   TYPE: DNA
;   ORGANISM: H. sapiens
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (38)...(1621)
US-09-356-806-7

  Query Match             79.1%;  Score 1354.2;  DB 4;  Length 2092;
  Best Local Similarity   88.8%;  Pred. No. 0;
  Matches 1522;  Conservative    0;  Mismatches  183;  Indels    8;  Gaps    5;

Qy          1 ATCGCATTGCACCAGGATGACTCTGAAATGGACTTCAGTTCTTCTGCTGATACATCTCCA 60
              || |||||||| |||||||  || ||||||||||||||| ||||||||||||||  |
Db         22 ATTGCATTGCATCAGGATGTCTATGAAATGGACTTCAGCTCTTCTGCTGATACAGCT-GA 80

Qy         61 GTTGTTACTTTAGCTCTGGGAGTTGTGGAAAAGTGCTGGTGTGGGCCGCAGAATACAGCC 120
              | |||||||||||||||||||||||||||||| |||||||||||  || |||||| |||||
Db         81 GCTGTTACTTTAGCTCTGGGAGTTGTGGAAAGGTGCTGGTGTGGCCCACAGAATTCAGCC 140

Qy        121 ATTGGATGAATATGAAGACAATCCTGAAAGAGCTTGTTCAGAGAGGTCATGAGGTGACTG 180
              | |||||||||| |||||||||||| | || ||||| |||||||||||||||||||||
Db        141 ACTGGATGAATATAAAGACAATCCTGGATGAACTTGTCCAGAGAGGTCATGAGGTGACTG 200

Qy        181 TACTGGCATCTTCAGCTTCCATTCTTTTTGATCCCAATGATGCATCCACTCTTAAATTTG 240
              || |||||||||||||||||||  ||| |||||||     |||| ||||||||||||||
Db        201 TATTGGCATCTTCAGCTTCCATTTCTTTCGATCCCAACAGCCCATCTACTCTTAAATTTG 260

Qy        241 AAGTTTATCCTACATCTTTAACTAAAACTGAATTTGAGAATATCATCATGCAACAGGTTA 300
              |||||||||||  |||||||||||||||||| |||||| |||| |||| ||| | ||||||
Db        261 AAGTTTATCCTGTATCTTTAACTAAAACTGAGTTTGAGGATATTATCAAGCAGCTGGTTA 320
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Qy       301 AGAGATGGTCAGACATTCGAAAAGATAGCTTTTGGTTATATTTTTCACAAGAACAAGAAA 360
Db       321 AGAGATGGGCAGAACTTCCAAAAGACACATTTTGGTCATATTTTTCACAAGTACAAGAAA 380

Qy       361 TCCTGTGGGAATTATATGACATATTTAGAAACTTCTGTAAAGATGTAGTTTCAAATAAGA 420
Db       381 TCATGTGGACATTTAATGACATACTTAGAAAGTTCTGTAAGGATATAGTTTCAAATAAGA 440

Qy       421 AAGTTATGAAAAAACTACAAGAGTCAAGATTTGACATCGTTTTTGCAGATGCTGTTTTTC 480
Db       441 AACTTATGAAGAAACTACAGGAGTCAAGATTTGATGTTGTTCTTGCAGATGCTGTTTTCC 500

Qy       481 CCTGTGGTGAGCTGCTGGCTGCGCTACTTAACATACGGTTTGTGTACAGTCTCCGCTTTA 540
Db       501 CCTTTGGTGAGCTGCTGGCCGAGTTACTTAAAATACCCTTTGTCTACAGCCTCCGCTTCT 560

Qy       541 CTCCTGGCTACACAATTGAAAGGCACAGTGGAGGACTGATTTTCCCTCCTTCCTACATAC 600
Db       561 CTCCTGGCTACGCAATTGAAAAGCATAGTGGAGGACTTCTGTTCCCTCCTTCCTATGTGC 620

Qy       601 CTATTGTTATGTCAAAATTAAGTGATCAAATGACTTTCATGGAGAGGGTAAAAAATATGA 660
Db       621 CTGTTGTTATGTCAGAACTAAGTGACCAAATGACTTTCATAGAGAGGGTAAAAAATATGA 680

Qy       661 TCTATGTGCTTTATTTTGACTTTTGGTTCCAAATGTCTGATATGAAGAAGTGGGATCAGT 720
Db       681 TCTATGTGCTTTATTTTGAATTTTGGTTCCAAATATTTGACATGAAGAAGTGGGATCAGT 740

Qy       721 TTTACAGTGAAGTTTTAGGAAGACCCACTACCTTATTTGAGACAATGGGAAAAGCTGACA 780
Db       741 TCTACAGTGAAGTTCTAGGAAGACCCACTACGTTATCTGAGACAATGGCAAAAGCTGACA 800

Qy       781 TATGGCTTATGCGAAACTCCTGGAGTTTTCAATTTCCTCATCCATTCTTACCAAACGTTG 840
Db       801 TATGGCTTATTCGAAACTACTGGGATTTTCAATTTCCTCACCCACTCTTACCAAATGTTG 860

Qy       841 ATTTTGTTGGAGGATTCCACTGGCAAACCTGCCAAACCCCTACCTAAGGAAATGGAGGAG 900
Db       861 AGTTCGTTGGAGGACTCCACT-GCAAACCTGCCAAACCCCTACCGAAGGAAATGGAAGAG 919

Qy       901 TTTGTACAGAGCTCTGGAGAAAATGGTGTTGTGGTGTTTTCTCTGGGGTCAGTGATAAGT 960
Db       920 TTTGTCCAGAGCTCTGGAGAAAATGGTGTTGTGGTGTTTTCTCTGGGGTCGATGGTCAGT 979

Qy       961 AACATGACAGCAGAAAGGGCCAATGTAATTGCAACAGCCCTTGCCAAGATCCCACAAAAG 1020
Db       980 AACACGTCAGAAGAAAGGGCCAATGTAATTGCATCAGCCCTTGCCAAGATCCCACAAAAG 1039

Qy      1021 GTTCTGTGGAGATTTGATGGGAATAAACCAGATGCCTTAGGTCTCAATACTCGGCTGTAT 1080
Db      1040 GTTCTGTGGAGATTTGATGGGAATAAACCAGATACTTTAGGACTCAATACTCGGCTGTAC 1099

Qy      1081 AAGTGGATACCCCAGAATGACCTTCTAGGTCATCCAAAAACCAGAGCTTTTATAACTCAT 1140
Db      1100 AAGTGGATACCCCAGAATGATCTTCTTGGTCACCCAAAAACCAGAGCTTTTATAACTCAT 1159

Qy      1141 GGTGGAGCCAATGGCATCTATGAGGCAATCTACCATGGGATCCCTATGGTGGGCATTCCA 1200
Db      1160 GGTGGAGCCAATGGCATCTATGAGGCAATCTACCATGGAATCCCTATGGTGGGCGTTCCA 1219

Qy      1201 TTGTTTTGGGATCAACCTGATAACATTGCTCACATGAAGGCCAAGGGAGCAGCTGTTAGA 1260
Db      1220 TTGTTTGCAGATCAACCTGATAACATTGCACACATGAAGGCCAAGGGAGCAGCTGTTAGT 1279

Qy      1261 TTGGACTTCAACACAATGTCGAGTACAGACCTGCTGAATGCACTGAAGACAGTAATTAAT 1320
Db      1280 TTGGACTTCCACACAATGTCGAGTACAGACTTACTCAATGCACTGAAGACAGTAATTAAT 1339

Qy      1321 GATCCTTTATATAAAGAGAATATTATGAAATTATCAAGAATTCAACATGATCAACCAGTA 1380
Db      1340 GATCCTTTATATAAAGAGAATGCTATGAAATTATCAAGAATTCATCATGATCAACCAGTG 1399

Qy      1381 AAGCCCCTGGATCGAGCAGTCTTCTGGATTGAATTTGTCATGCCCCACAAAGGAGCCAAA 1440
Db      1400 AAGCCCCTTGATCGAGCAGTCTTCTGGATTGAATTTGTCATGCGCCATAAAGGAGCCAAG 1459

Qy      1441 CACCTTCGAGTTGCAGCCCATGACCTCACCTGGTTCCAGTACCACTCTTTGGATGTGATT 1500
Db      1460 CACCTTCGGGTTGCAGCCCACGACCTCACCTGGTTCCAGTACCACTCTTTGGATGTGACT 1519

Qy      1501 GGGTTTCTGCTGGCCTGTGTGGCAACTGTGATATTTATCATCACAAAGTTTTGTCTGTTT 1560
Db      1520 GGGTTCCTGCTGGCCTGTGTGGCAACTGTGATATTCATCATCACAAA---ATGTCTGTTT 1576

Qy      1561 TGTTTCTGGAAGTTTGCTAGAAAAGGGAAGAAGGGAAAAAGAGATTAGTTATGTCTGACA 1620
Db      1577 TGTGTCTGGAAGTTTGTTAGAACAGGAAAGAAGGGGAAAAGAGATTAATTACGTCTGAGG 1636

Qy      1621 TTTGAAGCTGGAAAACCAGATAGATAGGACAACTTCAGTTTATTCCAGCAAGAAAGAAAA 1680
Db      1637 CTGGAAGCTGGGAAACCCAATAAAT-GAACTCCTTTAGTTTATTACAACAAGAA--GACG 1693

Qy      1681 GATTGTTATGCAAGATTTCTTTCTTCCTGTGAC 1713
Db      1694 TTGTGATACAAGAGATTCCTTTCTTCTTGTGAC 1726
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RESULT 6
US-09-949-016-2594
; Sequence 2594, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2594
; LENGTH: 2092
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-2594

Query Match 78.8%; Score 1349.4; DB 4; Length 2092;
Best Local Similarity 88.7%; Pred. No. 0;
Matches 1519; Conservative 0; Mismatches 186; Indels 8; Gaps 5;

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Qy          1 ATCGCATTGCACCAGGATGACTCTGAAATGGACTTCAGTTCTTCTGCTGATACATCTCCA 60
Db         22 ATTGCATTGCATCAGGATGTCTATGAAATGGACTTCAGCTCTTCTGCTGATACAGCT-GA 80

Qy         61 GTTGTTACTTTAGCTCTGGGAGTTGTGGAAAAGTGCTGGTGTGGGCCGCAGAATACAGCC 120
Db         81 GCTGTTACTTTAGCTCTGGGAGTTGTGGAAAGGTGCTGGTGTGGCCCACAGAATTCAGCC 140

Qy        121 ATTGGATGAATATGAAGACAATCCTGAAAGAGCTTGTTCAGAGAGGTCATGAGGTGACTG 180
Db        141 ACTGGATGAATATAAAGACAATCCTGGATGAACTTGTCCAGAGAGGTCATGAGGTGACTG 200

Qy        181 TACTGGCATCTTCAGCTTCCATTCTTTTTGATCCCAATGATGCATCCACTCTTAAATTTG 240
Db        201 TATTGGCATCTTCAGCTTCCATTTCTTTCGATCCCAACAGCCCATCTACTCTTAAATTTG 260

Qy        241 AAGTTTATCCTACATCTTTAACTAAAACTGAATTTGAGAATATCATCATGCAACAGGTTA 300
Db        261 AAGTTTATCCTGTATCTTTAACTAAAACTGAGTTTGAGGATATTATCAAGCAGCTGGTTA 320
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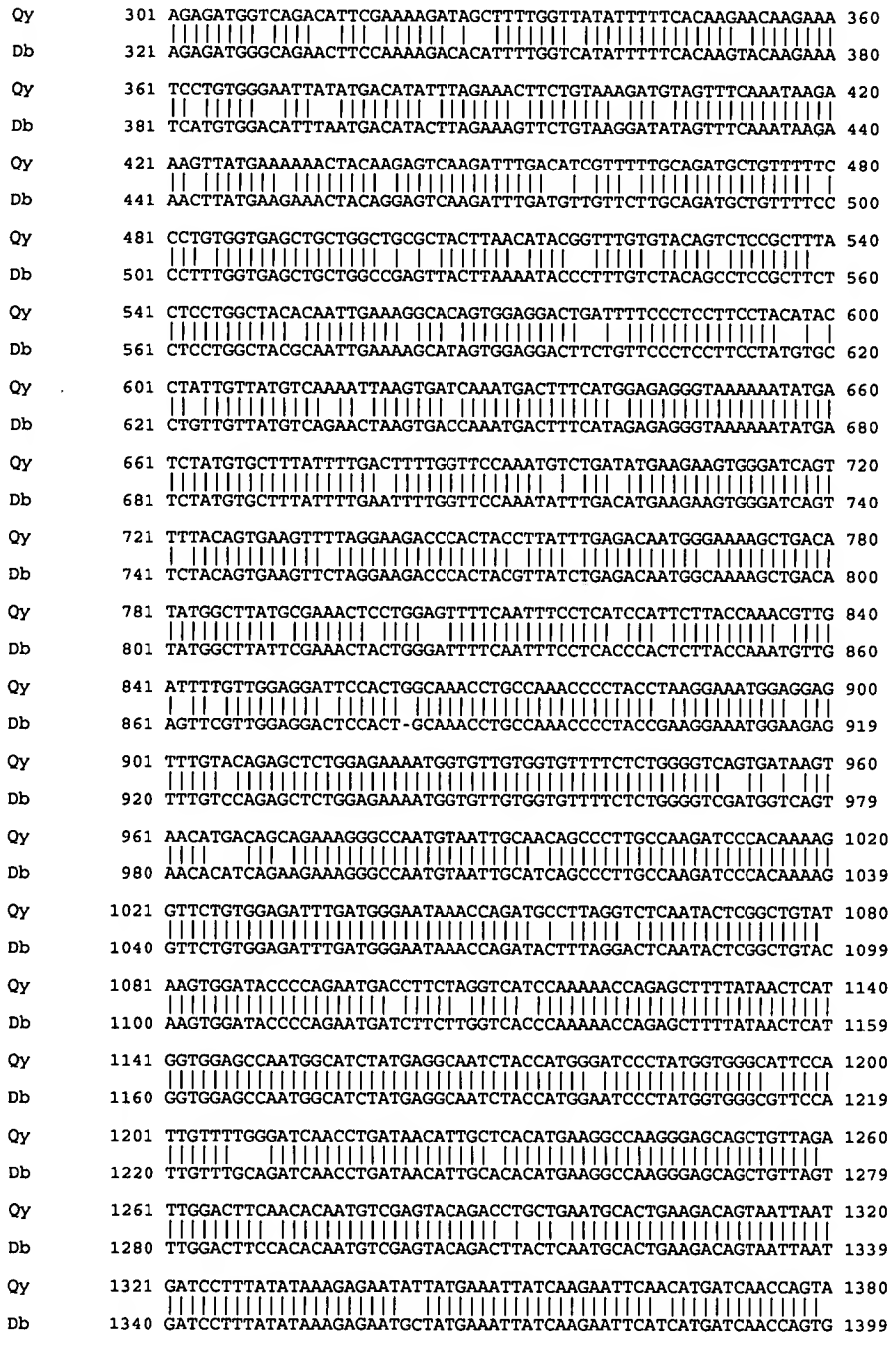
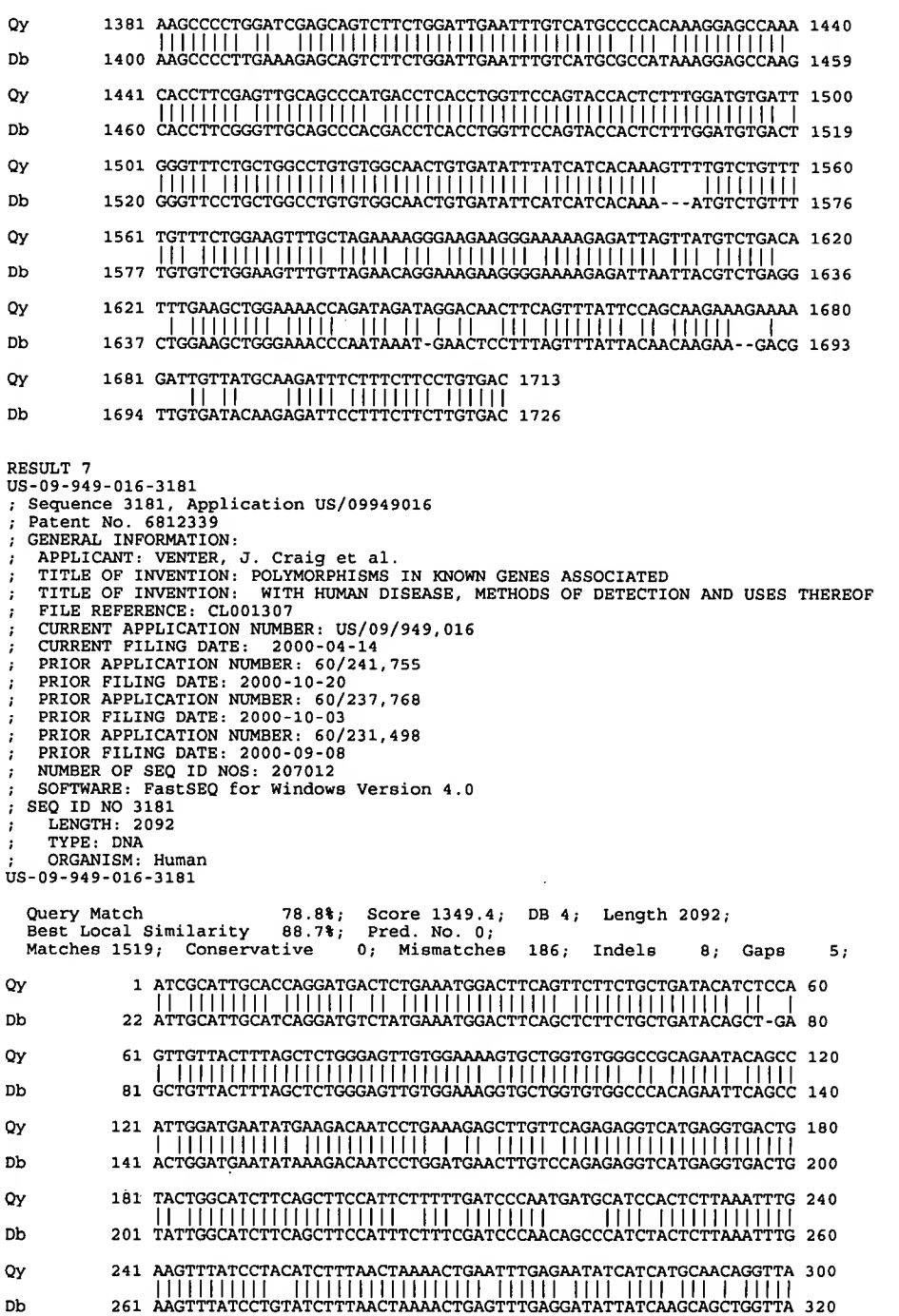
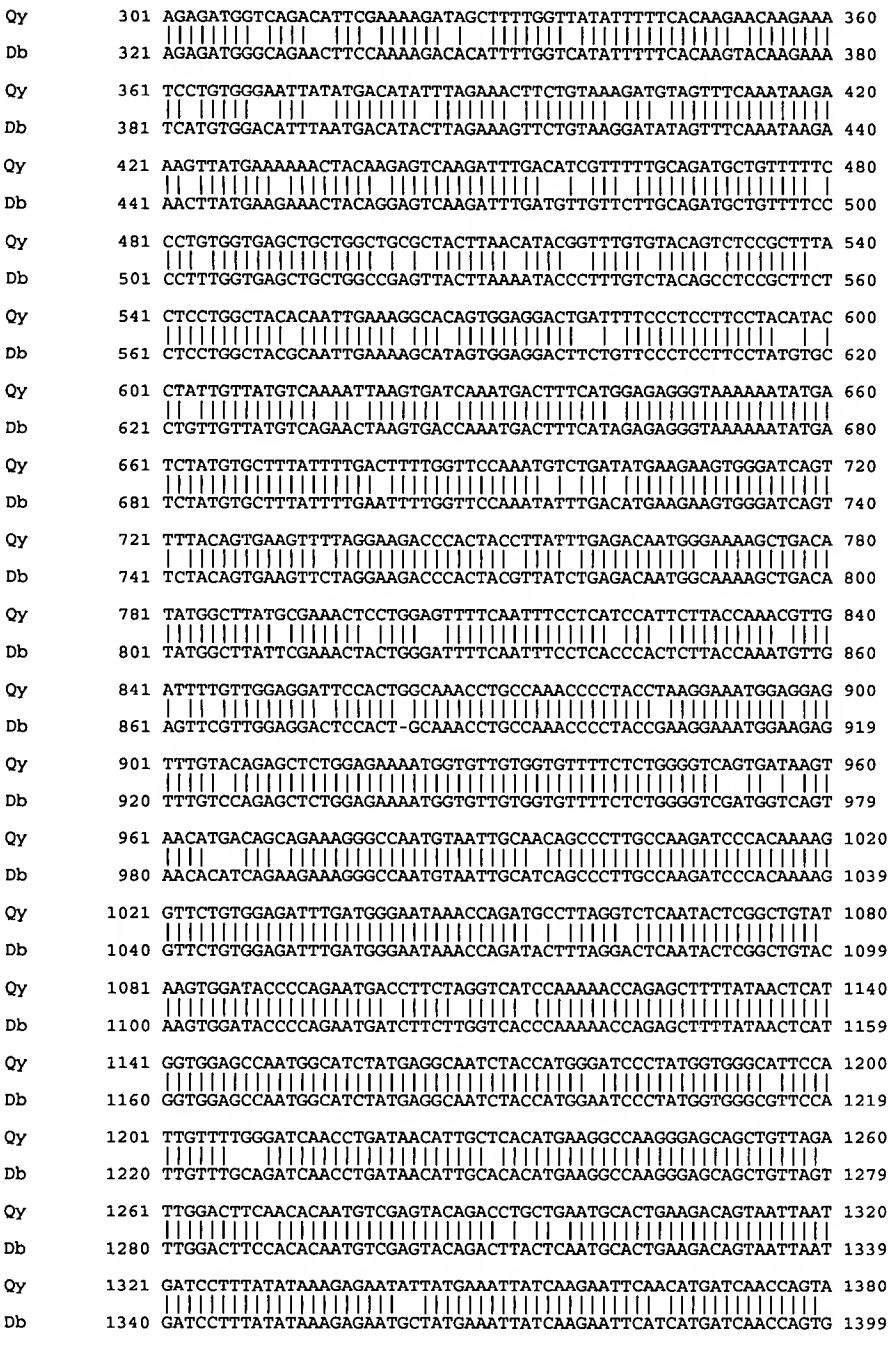
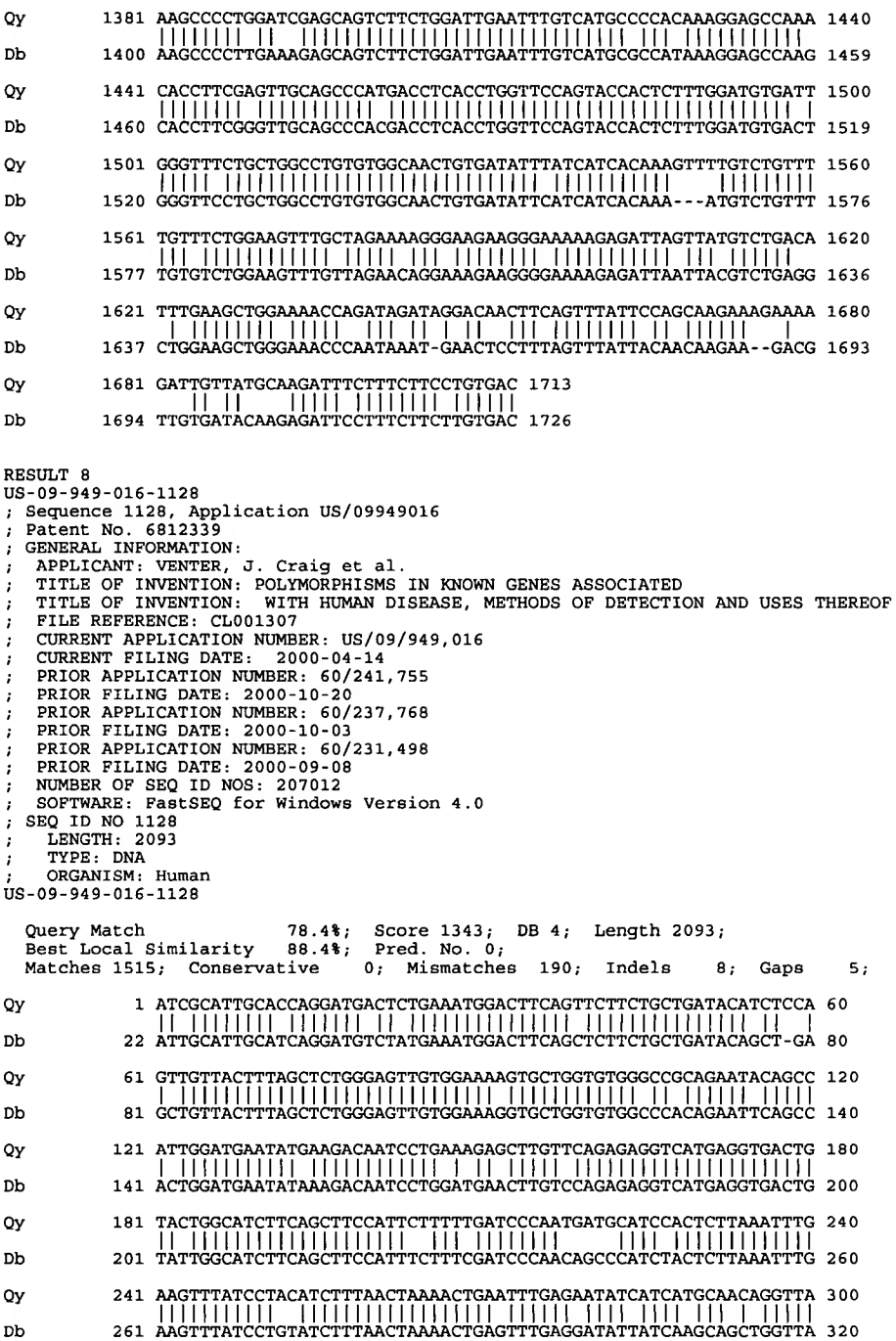




RESULT 7
US-09-949-016-3181
; Sequence 3181, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 3181
; LENGTH: 2092
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-3181

Query Match 78.8%; Score 1349.4; DB 4; Length 2092;
Best Local Similarity 88.7%; Pred. No. 0;
Matches 1519; Conservative 0; Mismatches 186; Indels 8; Gaps 5;





RESULT 8
US-09-949-016-1128
; Sequence 1128, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1128
; LENGTH: 2093
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-1128

Query Match 78.4%; Score 1343; DB 4; Length 2093;
Best Local Similarity 88.4%; Pred. No. 0;
Matches 1515; Conservative 0; Mismatches 190; Indels 8; Gaps 5;

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Qy       301 AGAGATGGTCAGACATTCGAAAAGATAGCTTTTGGTTATATTTTTCACAAGAACAAGAAA 360
Db       321 AGAGATGGGCAGAACTTCCAAAAGACACATTTTGGTCATATTTTTCACAAGTACAAGAAA 380

Qy       361 TCCTGTGGGAATTATATGACATATTTAGAAACTTCTGTAAAGATGTAGTTTCAAATAAGA 420
Db       381 TCATGTGGACATTTAATGACATACTTAGAAAGTTCTGTAAGGATATAGTTTCAAATAAGA 440

Qy       421 AAGTTATGAAAAAACTACAAGAGTCAAGATTTGACATCGTTTTTGCAGATGCTGTTTTTC 480
Db       441 AACTTATGAAGAAACTACAGGAGTCAAGATTTGATGTTGTTCTTGCAGATGCTGTTTTCC 500

Qy       481 CCTGTGGTGAGCTGCTGGCTGCGCTACTTAACATACGGTTTGTGTACAGTCTCCGCTTTA 540
Db       501 CCTTTGGTGAGCTGCTGGCCGAGTTACTTAAAATACCCTTTGTCTACAGGCCTCGCTTCT 560

Qy       541 CTCCTGGCTACACAATTGAAAGGCACAGTGGAGGACTGATTTTCCCTCCTTCCTACATAC 600
Db       561 CTCCTGGCTACGCAATTGAAAAGCATAGTGGAGGACTTCTGTTCCCTCCTTCCTATGTGC 620

Qy       601 CTATTGTTATGTCAAAATTAAGTGATCAAATGACTTTCATGGAGAGGGTAAAAAATATGA 660
Db       621 CTGTTGTTATGTCAGAACTAAGTGACCAAATGACTTTCATAGAGAGGGTAAAAAATATGA 680

Qy       661 TCTATGTGCTTTATTTTGACTTTTGGTTCCAAATGTCTGATATGAAGAAGTGGGATCAGT 720
Db       681 TCTATGTGCTTTATTTTGAATTTTGGTTCCAAATATTTGACATGAAGAAGTGGGATCAGT 740

Qy       721 TTTACAGTGAAGTTTTAGGAAGACCCACTACCTTATTTGAGACAATGGGAAAAGCTGACA 780
Db       741 TCTACAGTGAAGTTCTAGGAAGACCCACTACGTTATCTGAGACAATGGCAAAAGCTGACA 800

Qy       781 TATGGCTTATGCGAAACTCCTGGAGTTTTCAATTTCCTCATCCATTCTTACCAAACGTTG 840
Db       801 TATGGCTTATTCGAAACTACTGGGATTTTCAATTTCCTCACCCACTCTTACCAAATGTTG 860

Qy       841 ATTTTGTTGGAGGATTCCACTGGCAAACCTGCCAAACCCCTACCTAAGGAAATGGAGGAG 900
Db       861 AGTTCGTTGGAGGACTCCACT-GCAAACCTGCCAAACCCCTACCGAAGGAAATGGAAGAG 919

Qy       901 TTTGTACAGAGCTCTGGAGAAAATGGTGTTGTGGTGTTTTCTCTGGGGTCAGTGATAAGT 960
Db       920 TTTGTCCAGAGCTCTGGAGAAAATGGTGTTGTGGTGTTTTCTCTGGGGTCGATGGTCAGT 979

Qy       961 AACATGACAGCAGAAAGGGCCAATGTAATTGCAACAGCCCTTGCCAAGATCCCACAAAAG 1020
Db       980 AACACGTCAGAAGAAAGGGCCAATGTAATTGCATCAGCCCTTGCCAAGATCCCACAAAAG 1039

Qy      1021 GTTCTGTGGAGATTTGATGGGAATAAACCAGATGCCTTAGGTCTCAATACTCGGCTGTAT 1080
Db      1040 GTTCTGTGGAGATTTGATGGGAATAAACCAGATACTTTAGGACTCAATACTCGGCTGTAC 1099

Qy      1081 AAGTGGATACCCCAGAATGACCTTCTAGGTCATCCAAAAACCAGAGCTTTTATAACTCAT 1140
Db      1100 AAGTGGATACCCCAGAATGATCTTCTTGGTCACCCAAAAACCAGAGCTTTTATAACTCAT 1159

Qy      1141 GGTGGAGCCAATGGCATCTATGAGGCAATCTACCATGGGATCCCTATGGTGGGCATTCCA 1200
Db      1160 GGTGGAGCCAATGGCATCTATAAGGCAATCTCTCCTAGAATCCCTATGGTGGGCGTTCCA 1219

Qy      1201 TTGTTTTGGGATCAACCTGATAACATTGCTCACATGAAGGCCAAGGGAGCAGCTGTTAGA 1260
Db      1220 TTGTTTGCAGATCAACCTGATAACATTGCACACATGAAGGCCAAGGGAGCAGCTGTTAGT 1279

Qy      1261 TTGGACTTCAACACAATGTCGAGTACAGACCTGCTGAATGCACTGAAGACAGTAATTAAT 1320
Db      1280 TTGGACTTCCACACAATGTCGAGTACAGACTTACTCAATGCACTGAAGACAGTAATTAAT 1339

Qy      1321 GATCCTTTATATAAAGAGAATATTATGAAATTATCAAGAATTCAACATGATCAACCAGTA 1380
Db      1340 GATCCTTTATATAAAGAGAATGCTATGAAATTATCAAGAATTCATCATGATCAACCAGTG 1399

Qy      1381 AAGCCCCTGGATCGAGCAGTCTTCTGGATTGAATTTGTCATGCCCCACAAAGGAGCCAAA 1440
Db      1400 AAGCCCCTTGATCGAGCAGTCTTCTGGATTGAATTTGTCATGCGCCATAAAGGAGCCAAG 1459

Qy      1441 CACCTTCGAGTTGCAGCCCATGACCTCACCTGGTTCCAGTACCACTCTTTGGATGTGATT 1500
Db      1460 CACCTTCGGGTTGCAGCCCACGACCTCACCTGGTTCCAGTACCACTCTTTGGATGTGACT 1519

Qy      1501 GGGTTTCTGCTGGCCTGTGTGGCAACTGTGATATTTATCATCACAAAGTTTTGTCTGTTT 1560
Db      1520 GGGTTCCTGCTGGCCTGTGTGGCAACTGTGATATTCATCATCACAAA---ATGTCTGTTT 1576

Qy      1561 TGTTTCTGGAAGTTTGCTAGAAAAGGGAAGAAGGGAAAAAGAGATTAGTTATGTCTGACA 1620
Db      1577 TGTGTCTGGAAGTTTGTTAGAACAGGAAAGAAGGGGAAAAGAGATTAATTACGTCTGAGG 1636

Qy      1621 TTTGAAGCTGGAAAACCAGATAGATAGGACAACTTCAGTTTATTCCAGCAAGAAAGAAAA 1680
Db      1637 CTGGAAGCTGGGAAACCCAATAAAT-GAACTCCTTTAGTTTATTACAACAAGAA--GACG 1693

Qy      1681 GATTGTTATGCAAGATTTCTTTCTTCCTGTGAC 1713
Db      1694 TTGTGATACAAGAGATTCCTTTCTTCTTGTGAC 1726
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RESULT 9
US-09-180-852-1
; Sequence 1, Application US/09180852
; Patent No. 6287834
; GENERAL INFORMATION:
; APPLICANT: BELANGER, Alain
; APPLICANT: HUM, Dean W.
; APPLICANT: BEAULIEU, Martin
; APPLICANT: LEVESQUE, Eric
; TITLE OF INVENTION: CHARACTERIZATION AND USE OF AN ISOLATED URIDINE
; TITLE OF INVENTION: DIPHOSPHO-GLUCURONOSYLTRANSFERASE
; FILE REFERENCE: 1259-449
; CURRENT APPLICATION NUMBER: US/09/180,852
; CURRENT FILING DATE: 1999-02-08
; EARLIER APPLICATION NUMBER: PCT/CA97/00328
; EARLIER FILING DATE: 1997-05-16
; EARLIER APPLICATION NUMBER: US 08/649,319
; EARLIER FILING DATE: 1996-05-17
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 2107
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (52)..(1644)
US-09-180-852-1

Query Match 70.1%; Score 1201.6; DB 3; Length 2107;
Best Local Similarity 83.6%; Pred. No. 0;
Matches 1435; Conservative 0; Mismatches 269; Indels 12; Gaps 6;

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Db         36 ATTGCATAAGACCAGGATGTCTCTGAAATGGATGTCAGTCTTTCTGCTGATGCAGCT-CA 94

Qy         61 GTTGTTACTTTAGCTCTGGGAGTTGTGGAAAAGTGCTGGTGTGGGCCGCAGAATACAGCC 120
Db         95 GTTGTTACTTTAGCTCTGGGAGTTGTGGAAAGGTGCTGGTGTGGCCCACAGAATACAGCC 154

Qy        121 ATTGGATGAATATGAAGACAATCCTGAAAGAGCTTGTTCAGAGAGGTCATGAGGTGACTG 180
Db        155 ATTGGATAAATATGAAGACAATCCTGGAAGAGCTTGTTCAGAGGGGTCATGAGGTGATTG 214

Qy        181 TACTGGCATCTTCAGCTTCCATTCTTTTTGATCCCAATGATGCATCCACTCTTAAATTTG 240
Db        215 TGTTGACATCTTCGGCTTCTATTCTTGTCAATGCCAGTAAATCATCTGCTATTAAATTAG 274
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Qy       241 AAGTTTATCCTACATCTTTAACTAAAACTGAATTTGAGAATATCATCATGCAACAGGTTA 300
Db       275 AAGTTTATCCTACATCTTTAACTAAAAATGATTTGGAAGATTTTTTTATGAAAATGTTCG 334

Qy       301 AGAGATGGTCAGA---CATTCGAAAAGATAGCTTTTGGTTATATTTTTCACAAGAACAAG 357
Db       335 ATAGATGGACATATAGTATTTCAAAAAATACATTTTGGTCATATTTTTCACAACTACAAG 394

Qy       358 AAATCCTGTGGGAATTATATGACATATTTAGAAACTTCTGTAAAGATGTAGTTTCAAATA 417
Db       395 AATTGTGTTGGGAATATTCTGACTATAATATAAAGCTCTGTGAAGATGCAGTTTTGAACA 454

Qy       418 AGAAAGTTATGAAAAAACTACAAGAGTCAAGATTTGACATCGTTTTTGCAGATGCTGTTT 477
Db       455 AGAAACTTATGAGAAAACTACAAGAGTCAAAATTTGATGTCCTTCTGGCAGATGCCGTTA 514

Qy       478 TTCCCTGTGGTGAGCTGCTGGCTGCGCTACTTAACATACGGTTTGTGTACAGTCTCCGCT 537
Db       515 ATCCCTGTGGTGAGCTGCTGGCTGAACTACTTAACATACCCTTTCTGTACAGTCTCCGCT 574

Qy       538 TTACTCCTGGCTACACAATTGAAAGGCACAGTGGAGGACTGATTTTCCCTCCTTCCTACA 597
Db       575 TCTCTGTTGGCTACACAGTTGAGAAGAATGGTGGAGGATTTCTGTTCCCTCCTTCCTATG 634

Qy       598 TACCTATTGTTATGTCAAAATTAAGTGATCAAATGACTTTCATGGAGAGGGTAAAAAATA 657
Db       635 TACCTGTTGTTATGTCAGAATTAAGTGATCAAATGATTTTCATGGAGAGGATAAAAAATA 694

Qy       658 TGATCTATGTGCTTTATTTTGACTTTTGGTTCCAAATGTCTGATATGAAGAAGTGGGATC 717
Db       695 TGATATATATGCTTTATTTTGACTTTTGGTTTCAAGCATATGATCTGAAGAAGTGGGACC 754

Qy       718 AGTTTTACAGTGAAGTTTTAGGAAGACCCACTACCTTATTTGAGACAATGGGAAAAGCTG 777
Db       755 AGTTTTATAGTGAAGTTCTAGGAAGACCCACTACATTATTTGAGACAATGGGGAAAGCTG 814

Qy       778 ACATATGGCTTATGCGAAACTCCTGGAGTTTTCAATTTCCTCATCCATTCTTACCAAACG 837
Db       815 AAATGTGGCTCATTCGAACCTATTGGGATTTTGAATTTCCTCGCCCATTCTTACCAAATG 874

Qy       838 TTGATTTTGTTGGAGGATTCCACTGGCAAACCTGCCAAACCCCTACCTAAGGAAATGGAG 897
Db       875 TTGATTTTGTTGGAGGACTTCACT-GTAAACCAGCCAAACCCTTGCCTAAGGAAATGGAA 933

Qy       898 GAGTTTGTACAGAGCTCTGGAGAAAATGGTGTTGTGGTGTTTTCTCTGGGGTCAGTGATA 957
Db       934 GAGTTTGTGCAGAGCTCTGGAGAAAATGGTATTGTGGTGTTTTCTCTGGGGTCGATGATC 993

Qy       958 AGTAACATGACAGCAGAAAGGGCCAATGTAATTGCAACAGCCCTTGCCAAGATCCCACAA 1017
Db       994 AGTAACATGTCAGAAGAAAGTGCCAACATGATTGCATCAGCCCTTGCCCAGATCCCACAA 1053

Qy      1018 AAGGTTCTGTGGAGATTTGATGGGAATAAACCAGATGCCTTAGGTCTCAATACTCGGCTG 1077
Db      1054 AAGGTTCTATGGAGATTTGATGGCAAGAAGCCAAATACTTTAGGTTCCAATACTCGACTG 1113

Qy      1078 TATAAGTGGATACCCCAGAATGACCTTCTAGGTCATCCAAAAACCAGAGCTTTTATAACT 1137
Db      1114 TATAAGTGGTTACCCCAGAATGACCTTCTTGGTCATCCCAAAACCAAAGCTTTTATAACT 1173

Qy      1138 CATGGTGGAGCCAATGGCATCTATGAGGCAATCTACCATGGGATCCCTATGGTGGGCATT 1197
Db      1174 CATGGTGGAACCAATGGCATCTATGAGGCGATCTACCATGGGATCCCTATGGTGGGCATT 1233

Qy      1198 CCATTGTTTTGGGATCAACCTGATAACATTGCTCACATGAAGGCCAAGGGAGCAGCTGTT 1257
Db      1234 CCCTTGTTTGCGGATCAACATGATAACATTGCTCACATGAAAGCCAAGGGAGCAGCCCTC 1293

Qy      1258 AGATTGGACTTCAACACAATGTCGAGTACAGACCTGCTGAATGCACTGAAGACAGTAATT 1317
Db      1294 AGTGTGGACATCAGGACCATGTCAAGTAGAGATTTGCTCAATGCATTGAAGTCAGTCATT 1353

Qy      1318 AATGATCCTTTATATAAAGAGAATATTATGAAATTATCAAGAATTCAACATGATCAACCA 1377
Db      1354 AATGACCCTATCTATAAAGAGAATATCATGAAATTATCAAGAATTCATCATGATCAACCG 1413

Qy      1378 GTAAAGCCCCTGGATCGAGCAGTCTTCTGGATTGAATTTGTCATGCCCCACAAAGGAGCC 1437
Db      1414 GTGAAGCCCCTGGATCGAGCAGTCTTCTGGATTGAGTTTGTCATGCGCCATAAAGGAGCC 1473

Qy      1438 AAACACCTTCGAGTTGCAGCCCATGACCTCACCTGGTTCCAGTACCACTCTTTGGATGTG 1497
Db      1474 AAGCACCTTCGGGTCGCAGCCCACAACCTCACCTGGATCCAGTACCACTCTTTGGATGTG 1533

Qy      1498 ATTGGGTTTCTGCTGGCCTGTGTGGCAACTGTGATATTTATCATCACAAAGTTTTGTCTG 1557
Db      1534 ATAGCATTCCTGCTGGCCTGCGTGGCAACTATGATATTTATGATCACAAAATGTTGCCTG 1593

Qy      1558 TTTTGTTTCTGGAAGTTTGCTAGAAAAGGGAAGAAGGGAAAAAGAGATTAGTTATGTCTG 1617
Db      1594 TTTTGTTTCCGAAAGCTTGCCAAAACAGGAAAGAAGAAGAAAAGGGATTAGTTATATCAA 1653

Qy      1618 ACATTTGAAGCTGGAAAACCAGATAGATAGGACAACTTCAGTTTATTCCAGCAAGAAAGA 1677
Db      1654 AAGCCTGAAG-TGGAATGACCAAAAGATGGGACTCCTCC--TTTATTCCAGCATGGAGG- 1709

Qy      1678 AAAGATTGTTATGCAAGATTTCTTTCTTCCTGTGAC 1713
Db      1710 ---GTTTTAAATGGAGGATTTCCTTTTTCCTGCGAC 1742
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RESULT 10
US-09-356-806-112
; Sequence 112, Application US/09356806
; Patent No. 6586175
; GENERAL INFORMATION:
; APPLICANT: Penny, Laura
; APPLICANT: Galvin, Margaret
; APPLICANT: Miller, Andrew
; APPLICANT: Reidy, Michael
; TITLE OF INVENTION: Genotyping Human
; TITLE OF INVENTION: UDP-Glucuronosyltransferase 2B4 (UGT2B4), 2B7 (UGT2B7) and
; TITLE OF INVENTION: 2B15 (UGT2B15) Genes
; FILE REFERENCE: SEQ-22PRV2
; CURRENT APPLICATION NUMBER: US/09/356,806
; CURRENT FILING DATE: 1999-07-20
; NUMBER OF SEQ ID NOS: 164
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 112
; LENGTH: 1976
; TYPE: DNA
; ORGANISM: H. sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (11)...(1598)
US-09-356-806-112

Query Match 69.4%; Score 1188.8; DB 4; Length 1976;
Best Local Similarity 83.1%; Pred. No. 0;
Matches 1417; Conservative 0; Mismatches 277; Indels 12; Gaps 5;

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Qy        11 ACCAGGATGACTCTGAAATGGACTTCAGTTCTTCTGCTGATACATCTCCAGTTGTTACTT 70
Db         5 ACCAGGATGTCTCTGAAATGGACGTCAGTCTTTCTGCTGATACAGCT-CAGTTGTTACTT 63

Qy        71 TAGCTCTGGGAGTTGTGGAAAAGTGCTGGTGTGGGCCGCAGAATACAGCCATTGGATGAA 130
Db        64 TAGCTCTGGAAGCTGTGGAAAGGTGCTAGTGTGGCCCACAGAATACAGCCATTGGATAAA 123

Qy       131 TATGAAGACAATCCTGAAAGAGCTTGTTCAGAGAGGTCATGAGGTGACTGTACTGGCATC 190
Db       124 TATGAAGACAATCCTGGAAGAGCTTGTTCAGAGGGGTCATGAGGTGACTGTGTTGACATC 183

Qy       191 TTCAGCTTCCATTCTTTTTGATCCCAATGATGCATCCACTCTTAAATTTGAAGTTTATCC 250
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Db        184 TTCGGCTTCTACTCTTGTCAATGCCAGTAAATCATCTGCTATTAAATTAGAAGTTTATCC 243
Qy        251 TACATCTTTAACTAAAACTGAATTTGAGAATATCATCATGCAACAGGTTAAGAGATGG-- 308
Db        244 TACATCTTTAACTAAAAATGATTTGGAAGATTCTCTTCTGAAAATTCTCGATAGATGGAT 303
Qy        309 -TCAGACATTCGAAAAGATAGCTTTTGGTTATATTTTTCACAAGAACAAGAAATCCTGTG 367
Db        304 ATATGGTGTTTCAAAAAATACATTTTGGTCATATTTTTCACAATTACAAGAATTGTGTTG 363
Qy        368 GGAATTATATGACATATTTAGAAACTTCTGTAAAGATGTAGTTTCAAATAAGAAAGTTAT 427
Db        364 GGAATATTATGACTACAGTAACAAGCTCTGTAAAGATGCAGTTTTGAATAAGAAACTTAT 423
Qy        428 GAAAAAACTACAAGAGTCAAGATTTGACATCGTTTTTGCAGATGCTGTTTTTCCCTGTGG 487
Db        424 GATGAAACTACAAGAGTCAAAGTTTGATGTCATTCTGGCAGATGCCCTTAATCCCTGTGG 483
Qy        488 TGAGCTGCTGGCTGCGCTACTTAACATACGGTTTGTGTACAGTCTCCGCTTTACTCCTGG 547
Db        484 TGAGCTACTGGCTGAACTATTTAACATACCCTTTCTGTACAGTCTTCGATTCTCTGTTGG 543
Qy        548 CTACACAATTGAAAGGCACAGTGGAGGACTGATTTTCCCTCCTTCCTACATACCTATTGT 607
Db        544 CTACACATTTGAGAAGAATGGTGGAGGATTTCTGTTCCCTCCTTCCTATGTACCTGTTGT 603
Qy        608 TATGTCAAAATTAAGTGATCAAATGACTTTCATGGAGAGGGTAAAAAATATGATCTATGT 667
Db        604 TATGTCAGAATTAAGTGATCAAATGATTTTCATGGAGAGGATAAAAAATATGATACATAT 663
Qy        668 GCTTTATTTTGACTTTTGGTTCCAAATGTCTGATATGAAGAAGTGGGATCAGTTTTACAG 727
Db        664 GCTTTATTTTGACTTTTGGTTTCAAATTTATGATCTGAAGAAGTGGGACCAGTTTTATAG 723
Qy        728 TGAAGTTTTAGGAAGACCCACTACCTTATTTGAGACAATGGGGAAAAGCTGACATATGGCT 787
Db        724 TGAAGTTCTAGGAAGACCCACTACATTATTTGAGACAATGGGGAAAGCTGAAATGTGGCT 783
Qy        788 TATGCGAAACTCCTGGAGTTTTCAATTTCCTCATCCATTCTTACCAAACGTTGATTTTGT 847
Db        784 CATTCGAACCTATTGGGATTTTGAATTTCCTCGCCCATTCTTACCAAATGTTGATTTTGT 843
Qy        848 TGGAGGATTCCACTGGCAAACCTGCCAAACCCCTACCTAAGGAAATGGAGGAGTTTGTAC 907
Db        844 TGGAGGACTTCACT-GTAAACCAGCCAAACCCCTGCCTAAGGAAATGGAAGAGTTTGTGC 902
Qy        908 AGAGCTCTGGAGAAAATGGTGTTGTGGTGTTTTCTCTGGGGTCAGTGATAAGTAACATGA 967
Db        903 AGAGCTCTGGAGAAAATGGTATTGTGGTGTTTTCTCTGGGGTCGATGATCAGTAACATGT 962
Qy        968 CAGCAGAAAGGGCCAATGTAATTGCAACAGCCCTTGCCAAGATCCCACAAAAGGTTCTGT 1027
Db        963 CAGAAGAAAGTGCCAACATGATTGCATCAGCCCTTGCCCAGATCCCACAAAAGGTTCTAT 1022
Qy       1028 GGAGATTTGATGGGAATAAACCAGATGCCTTAGGTCTCAATACTCGGCTGTATAAGTGGA 1087
Db       1023 GGAGATTTGATGGCAAGAAGCCAAATACTTTAGGTTCCAATACTCGACTGTACAAGTGGT 1082
Qy       1088 TACCCCAGAATGACCTTCTAGGTCATCCAAAAACCAGAGCTTTTATAACTCATGGTGGAG 1147
Db       1083 TACCCCAGAATGACCTTCTTGGTCATCCCAAAACCAAAGCTTTTATAACTCATGGTGGAA 1142
Qy       1148 CCAATGGCATCTATGAGGCAATCTACCATGGGATCCCTATGGTGGGCATTCCATTGTTTT 1207
Db       1143 CCAATGGCATCTATGAGGCGATCTACCATGGGATCCCTATGGTGGGCATTCCCTTGTTTG 1202
Qy       1208 GGGATCAACCTGATAACATTGCTCACATGAAGGCCAAGGGAGCAGCTGTTAGATTGGACT 1267
Db       1203 CGGATCAACATGATAACATTGCTCACATGAAAGCCAAGGGAGCAGCCCTCAGTGTGGACA 1262
Qy       1268 TCAACACAATGTCGAGTACAGACCTGCTGAATGCACTGAAGACAGTAATTAATGATCCTT 1327
Db       1263 TCAGGACCATGTCAAGTAGAGATTTGCTCAATGCATTGAAGTCAGTCATTAATGACCCTG 1322

Qy       1328 TATATAAAGAGAATATTATGAAATTATCAAGAATTCAACATGATCAACCAGTAAAGCCCC 1387
Db       1323 TCTATAAAGAGAATGTCATGAAATTATCAAGAATTCATCATGACCAACCAATGAAGCCCC 1382
Qy       1388 TGGATCGAGCAGTCTTCTGGATTGAATTTGTCATGCCCCACAAAGGAGCCAAACACCTTC 1447
Db       1383 TGGATCGAGCAGTCTTCTGGATTGAGTTTGTCATGCGCCACAAAGGAGCCAAGCACCTTC 1442
Qy       1448 GAGTTGCAGCCCATGACCTCACCTGGTTCCAGTACCACTCTTTGGATGTGATTGGGTTTC 1507
Db       1443 GAGTCGCAGCTCACAACCTCACCTGGATCCAGTACCACTCTTTGGATGTGATAGCATTCC 1502
Qy       1508 TGCTGGCCTGTGTGGCAACTGTGATATTTATCATCACAAAGTTTTGTCTGTTTTGTTTCT 1567
Db       1503 TGCTGGCCTGCGTGGCAACTGTGATATTTATCATCACAAAATTTTGCCTGTTTTGTTTCC 1562
Qy       1568 GGAAGTTTGCTAGAAAAGGGAAGAAGGGAAAAAGAGATTAGTTATGTCTGACATTTGAAG 1627
Db       1563 GAAAGCTTGCCAAAACAGGAAAGAAGAAGAAAAGAGATTAGTTATATCAAAAGCCTGAAG 1622
Qy       1628 CTGGAAAACCAGATAGATAGGACAACTTCAGTTTATTCCAGCAAGAAAGAAAAGATTGTT 1687
Db       1623 -TGGAATGACTGAAAGATGGGACTCCTCCTTTATTT------CAGCATGGAGGGTTTTAA 1675
Qy       1688 ATGCAAGATTTCTTTCTTCCTGTGAC 1713
Db       1676 ATGGAGGATTTCCTTTTTCCTGTGAC 1701
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RESULT 11
US-09-813-918-1
; Sequence 1, Application US/09813918
; Patent No. 6383789
; GENERAL INFORMATION:
; APPLICANT: WEBSTER, Marion et al.
; TITLE OF INVENTION: ISOLATED HUMAN DRUG-METABOLIZING
; TITLE OF INVENTION: PROTEINS, NUCLEIC ACID MOLECULES ENCODING HUMAN
; TITLE OF INVENTION: DRUG-METABOLIZING PROTEINS,
; TITLE OF INVENTION: AND USES THEREOF
; FILE REFERENCE: CL001175
; CURRENT APPLICATION NUMBER: US/09/813,918
; CURRENT FILING DATE: 2001-03-22
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 1413
; TYPE: DNA
; ORGANISM: Human
US-09-813-918-1

Query Match 65.9%; Score 1128.8; DB 3; Length 1413;
Best Local Similarity 85.4%; Pred. No. 0;
Matches 1393; Conservative 0; Mismatches 12; Indels 227; Gaps 3;

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Qy           1 ATCGCATTGCACCAGGATGACTCTGAAATGGACTTCAGTTCTTCTGCTGATACATCTCCA 60
Db           7 ATCACATTGCACCAGGATGACTCTGAAATGGACTTCAGTTCTCCTGCTGATACATCT-CA 65
Qy          61 GTTGTTACTTTAGCTCTGGGAGTTGTGGAAAAGTGCTGGTGTGGGCCGCAGAATACAGCC 120
Db          66 GTTGTTACTTTAGCTCTGGGAGTTGTGGAAAAGTGCTGGTGTGGGCCGCAGAATACAGCC 125
Qy         121 ATTGGATGAATATGAAGACAATCCTGAAAGAGCTTGTTCAGAGAGGTCATGAGGTGACTG 180
Db         126 ATTGGATGAATATGAAGACAATCCTGAAAGAGCTTGTTCAGAGAGGTCATGAGGTGACTG 185
Qy         181 TACTGGCATCTTCAGCTTCCATTCTTTTTGATCCCAATGATGCATCCACTCTTAAATTTG 240
Db         186 TACTGGCATCTTCAGCTTCCATTCTTTTTGATCCCAATGATGCATCCACTCTTAAATTTG 245
Qy         241 AAGTTTATCCTACATCTTTAACTAAAACTGAATTTGAGAATATCATCATGCAACAGGTTA 300
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Db        246 AAGTTTATCCTACATCTTTAACTAAAACTGAATTTGAGAATATCATCATGCAACAGGTTA 305
Qy        301 AGAGATGGTCAGACATTCGAAAAGATAGCTTTTGGTTATATTTTTCACAAGAACAAGAAA 360
Db        306 AGAGATGGTCAGACATTCGAAAAGATAGCTTTTGGTTATATTTTTCACAAGAACAAGAAA 365
Qy        361 TCCTGTGGGAATTATATGACATATTTAGAAACTTCTGTAAAGATGTAGTTTCAAATAAGA 420
Db        366 TCCTGTGGGAATTATATGACATATTTAGAAACTTCTGTAAAGATGTAGTTTCAAATAAGA 425
Qy        421 AAGTTATGAAAAAACTACAAGAGTCAAGATTTGACATCGTTTTTGCAGATGCTGTTTTTC 480
Db        426 AAGTTATGAAAAAACTACAAGAGTTAAGATTTGACATCGTTTTTGCAGATGCTGTTTTTC 485
Qy        481 CCTGTGGTGAGCTGCTGGCTGCGCTACTTAACATACGGTTTGTGTACAGTCTCCGCTTTA 540
Db        486 CCTGTGGTGAGCTGCTGGCTGCGCTACTTAACATAC---------------------- 521
Qy        541 CTCCTGGCTACACAATTGAAAGGCACAGTGGAGGACTGATTTTCCCTCCTTCCTACATAC 600
Db        522 ------------------------------------------------------------ 521
Qy        601 CTATTGTTATGTCAAAATTAAGTGATCAAATGACTTTCATGGAGAGGGTAAAAAATATGA 660
Db        522 ------------------------------------------------------------ 521
Qy        661 TCTATGTGCTTTATTTTGACTTTTGGTTCCAAATGTCTGATATGAAGAAGTGGGATCAGT 720
Db        522 ------------------------------------------------------------ 521
Qy        721 TTTACAGTGAAGTTTTAGGAAGACCCACTACCTTATTTGAGACAATGGGAAAAGCTGACA 780
Db        522 --------------------GACCCACTACCTTATTTGAGACAATGGGAAAAGCTGACA 560
Qy        781 TATGGCTTATGCGAAACTCCTGGAGTTTTCAATTTCCTCATCCATTCTTACCAAACGTTG 840
Db        561 TATGGCTTATGCGAAACCCCTGGAGTTTTCAATTTCCTCATCCATTCTTACCAAACGTTG 620
Qy        841 ATTTTGTTGGAGGATTCCACTGGCAAACCTGCCAAACCCCTACCTAAGGAAATGGAGGAG 900
Db        621 ATTTTGTTGGAGGATTCCACT-GCAAACCTGCCAAACCCCTACCTAAGGAAATGGAGGAG 679
Qy        901 TTTGTACAGAGCTCTGGAGAAAATGGTGTTGTGGTGTTTTCTCTGGGGTCAGTGATAAGT 960
Db        680 TTTGTACAGAGCTCTGGAGAAAATGGTGTTGTGGTGTTTTCTCTGGGGTCAGTGATAAGT 739
Qy        961 AACATGACAGCAGAAAGGGCCAATGTAATTGCAACAGCCCTTGCCAAGATCCCACAAAAG 1020
Db        740 AACATGACAGCAGAAAGGGCCAATGTAATTGCAACAGCCCTTGCCAGGATCCCACAAAAG 799
Qy       1021 GTTCTGTGGAGATTTGATGGGAATAAACCAGATGCCTTAGGTCTCAATACTCGGCTGTAT 1080
Db        800 GTTCTGTGGAGATTTGACGGGAATAAACCAGATGCCTTAGGTCTCAATACTCGGCTGTAC 859
Qy       1081 AAGTGGATACCCCAGAATGACCTTCTAGGTCATCCAAAAACCAGAGCTTTTATAACTCAT 1140
Db        860 AAGTGGATACCCCAGAATGACCTTCTAGGTCATCCAAAAACCAGAGCTTTTATAACTCAT 919
Qy       1141 GGTGGAGCCAATGGCATCTATGAGGCAATCTACCATGGGATCCCTATGGTGGGCATTCCA 1200
Db        920 GGTGGAGCCAATGGCATCTATGAGGCAATCTACCATGGGATCCCCATGGTGGGCATTCCA 979
Qy       1201 TTGTTTTGGGATCAACCTGATAACATTGCTCACATGAAGGCCAAGGGAGCAGCTGTTAGA 1260
Db        980 TTGTTTTTTGATCAACCTGATAACATTGCTCACATGAAGGCCAAGGGAGCAGCTGTTAGA 1039
Qy       1261 TTGGACTTCAACACAATGTCGAGTACAGACCTGCTGAATGCACTGAAGACAGTAATTAAT 1320
Db       1040 TTGGACTTCAACACAATGTCGAGTACAGACCTGCTGAATGCACTGAAGACAGTAATTAAT 1099
Qy       1321 GATCCTTTATATAAAGAGAATATTATGAAATTATCAAGAATTCAACATGATCAACCAGTA 1380
Db       1100 GATCCTTTATATAAAGAGAATATTATGAAATTATCAAGAATTCAACATGATCAACCAGTA 1159
Qy       1381 AAGCCCCTGGATCGAGCAGTCTTCTGGATTGAATTTGTCATGCCCCACAAAGGAGCCAAA 1440
Db       1160 AAGCCCCTGGATCGAGCAGTCTTCTGGATTGAATTTGTCATGCCCCACAAAGGAGCCAAA 1219
Qy       1441 CACCTTCGAGTTGCAGCCCATGACCTCACCTGGTTCCAGTACCACTCTTTGGATGTGATT 1500
Db       1220 CACCTTCGAGTTGCAGCCCATGACCTCACCTGGTTCCAGTACCACTCTTTGGATGTGATT 1279
Qy       1501 GGGTTTCTGCTGGCCTGTGTGGCAACTGTGATATTTATCATCACAAAGTTTTGTCTGTTT 1560
Db       1280 GGGTTTCTGCTGGCCTGTGTGGCAACTGTGATATTTATCATCACAAAGTTTTGTCTGTTT 1339
Qy       1561 TGTTTCTGGAAGTTTGCTAGAAAAGGGAAGAAGGGAAAAAGAGATTAGTTATGTCTGACA 1620
Db       1340 TGTTTCTGGAAGTTTGCTAGAAAAGGGAAGAAGGGAAAAAGAGATTAGTTATGTCCGACA 1399
Qy       1621 TTTGAAGCTGGA 1632
Db       1400 TTTGAAGCTGAA 1411
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RESULT 12
US-10-060-311-1
; Sequence 1, Application US/10060311
; Patent No. 6713295
; GENERAL INFORMATION:
; APPLICANT: WEBSTER, Marion et al.
; TITLE OF INVENTION: ISOLATED HUMAN DRUG-METABOLIZING
; TITLE OF INVENTION: PROTEINS, NUCLEIC ACID MOLECULES ENCODING HUMAN
; TITLE OF INVENTION: DRUG-METABOLIZING PROTEINS, AND USES THEREOF
; FILE REFERENCE: CL001175DIV
; CURRENT APPLICATION NUMBER: US/10/060,311
; CURRENT FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 1413
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-060-311-1

Query Match 65.9%; Score 1128.8; DB 4; Length 1413;
Best Local Similarity 85.4%; Pred. No. 0;
Matches 1393; Conservative 0; Mismatches 12; Indels 227; Gaps 3;

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Qy          1 ATCGCATTGCACCAGGATGACTCTGAAATGGACTTCAGTTCTTCTGCTGATACATCTCCA 60
Db          7 ATCACATTGCACCAGGATGACTCTGAAATGGACTTCAGTTCTCCTGCTGATACATCT-CA 65
Qy         61 GTTGTTACTTTAGCTCTGGGAGTTGTGGAAAAGTGCTGGTGTGGGCCGCAGAATACAGCC 120
Db         66 GTTGTTACTTTAGCTCTGGGAGTTGTGGAAAAGTGCTGGTGTGGGCCGCAGAATACAGCC 125
Qy        121 ATTGGATGAATATGAAGACAATCCTGAAAGAGCTTGTTCAGAGAGGTCATGAGGTGACTG 180
Db        126 ATTGGATGAATATGAAGACAATCCTGAAAGAGCTTGTTCAGAGAGGTCATGAGGTGACTG 185
Qy        181 TACTGGCATCTTCAGCTTCCATTCTTTTTGATCCCAATGATGCATCCACTCTTAAATTTG 240
Db        186 TACTGGCATCTTCAGCTTCCATTCTTTTTGATCCCAATGATGCATCCACTCTTAAATTTG 245
Qy        241 AAGTTTATCCTACATCTTTAACTAAAACTGAATTTGAGAATATCATCATGCAACAGGTTA 300
Db        246 AAGTTTATCCTACATCTTTAACTAAAACTGAATTTGAGAATATCATCATGCAACAGGTTA 305
Qy        301 AGAGATGGTCAGACATTCGAAAAGATAGCTTTTGGTTATATTTTTCACAAGAACAAGAAA 360
Db        306 AGAGATGGTCAGACATTCGAAAAGATAGCTTTTGGTTATATTTTTCACAAGAACAAGAAA 365
Qy        361 TCCTGTGGGAATTATATGACATATTTAGAAACTTCTGTAAAGATGTAGTTTCAAATAAGA 420
Db        366 TCCTGTGGGAATTATATGACATATTTAGAAACTTCTGTAAAGATGTAGTTTCAAATAAGA 425
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Qy       421 AAGTTATGAAAAAACTACAAGAGTCAAGATTTGACATCGTTTTTGCAGATGCTGTTTTTC 480
Db       426 AAGTTATGAAAAAACTACAAGAGTTAAGATTTGACATCGTTTTTGCAGATGCTGTTTTTC 485

Qy       481 CCTGTGGTGAGCTGCTGGCTGCGCTACTTAACATACGGTTTGTGTACAGTCTCCGCTTTA 540
Db       486 CCTGTGGTGAGCTGCTGGCTGCGCTACTTAACATAC---------------------- 521

Qy       541 CTCCTGGCTACACAATTGAAAGGCACAGTGGAGGACTGATTTTCCCTCCTTCCTACATAC 600
Db       522 ------------------------------------------------------------ 521

Qy       601 CTATTGTTATGTCAAAATTAAGTGATCAAATGACTTTCATGGAGAGGGTAAAAAATATGA 660
Db       522 ------------------------------------------------------------ 521

Qy       661 TCTATGTGCTTTATTTTGACTTTTGGTTCCAAATGTCTGATATGAAGAAGTGGGATCAGT 720

Qy       721 TTTACAGTGAAGTTTTAGGAAGACCCACTACCTTATTTGAGACAATGGGAAAAGCTGACA 780
Db       522 --------------------GACCCACTACCTTATTTGAGACAATGGGAAAAGCTGACA 560

Qy       781 TATGGCTTATGCGAAACTCCTGGAGTTTTCAATTTCCTCATCCATTCTTACCAAACGTTG 840
Db       561 TATGGCTTATGCGAAACCCCTGGAGTTTTCAATTTCCTCATCCATTCTTACCAAACGTTG 620

Qy       841 ATTTTGTTGGAGGATTCCACTGGCAAACCTGCCAAACCCCTACCTAAGGAAATGGAGGAG 900
Db       621 ATTTTGTTGGAGGATTCCACT-GCAAACCTGCCAAACCCCTACCTAAGGAAATGGAGGAG 679

Qy       901 TTTGTACAGAGCTCTGGAGAAAATGGTGTTGTGGTGTTTTCTCTGGGGTCAGTGATAAGT 960
Db       680 TTTGTACAGAGCTCTGGAGAAAATGGTGTTGTGGTGTTTTCTCTGGGGTCAGTGATAAGT 739

Qy       961 AACATGACAGCAGAAAGGGCCAATGTAATTGCAACAGCCCTTGCCAAGATCCCACAAAAG 1020
Db       740 AACATGACAGCAGAAAGGGCCAATGTAATTGCAACAGCCCTTGCCAGGATCCCACAAAAG 799

Qy      1021 GTTCTGTGGAGATTTGATGGGAATAAACCAGATGCCTTAGGTCTCAATACTCGGCTGTAT 1080
Db       800 GTTCTGTGGAGATTTGACGGGAATAAACCAGATGCCTTAGGTCTCAATACTCGGCTGTAC 859

Qy      1081 AAGTGGATACCCCAGAATGACCTTCTAGGTCATCCAAAAACCAGAGCTTTTATAACTCAT 1140
Db       860 AAGTGGATACCCCAGAATGACCTTCTAGGTCATCCAAAAACCAGAGCTTTTATAACTCAT 919

Qy      1141 GGTGGAGCCAATGGCATCTATGAGGCAATCTACCATGGGATCCCTATGGTGGGCATTCCA 1200
Db       920 GGTGGAGCCAATGGCATCTATGAGGCAATCTACCATGGGATCCCCATGGTGGGCATTCCA 979

Qy      1201 TTGTTTTGGGATCAACCTGATAACATTGCTCACATGAAGGCCAAGGGAGCAGCTGTTAGA 1260
Db       980 TTGTTTTTTGATCAACCTGATAACATTGCTCACATGAAGGCCAAGGGAGCAGCTGTTAGA 1039

Qy      1261 TTGGACTTCAACACAATGTCGAGTACAGACCTGCTGAATGCACTGAAGACAGTAATTAAT 1320
Db      1040 TTGGACTTCAACACAATGTCGAGTACAGACCTGCTGAATGCACTGAAGACAGTAATTAAT 1099

Qy      1321 GATCCTTTATATAAAGAGAATATTATGAAATTATCAAGAATTCAACATGATCAACCAGTA 1380
Db      1100 GATCCTTTATATAAAGAGAATATTATGAAATTATCAAGAATTCAACATGATCAACCAGTA 1159

Qy      1381 AAGCCCCTGGATCGAGCAGTCTTCTGGATTGAATTTGTCATGCCCCACAAAGGAGCCAAA 1440
Db      1160 AAGCCCCTGGATCGAGCAGTCTTCTGGATTGAATTTGTCATGCCCCACAAAGGAGCCAAA 1219

Qy      1441 CACCTTCGAGTTGCAGCCCATGACCTCACCTGGTTCCAGTACCACTCTTTGGATGTGATT 1500
Db      1220 CACCTTCGAGTTGCAGCCCATGACCTCACCTGGTTCCAGTACCACTCTTTGGATGTGATT 1279

Qy      1501 GGGTTTCTGCTGGCCTGTGTGGCAACTGTGATATTTATCATCACAAAGTTTTGTCTGTTT 1560
Db      1280 GGGTTTCTGCTGGCCTGTGTGGCAACTGTGATATTTATCATCACAAAGTTTTGTCTGTTT 1339

Qy      1561 TGTTTCTGGAAGTTTGCTAGAAAAGGGAAGAAGGGAAAAAGAGATTAGTTATGTCTGACA 1620
Db      1340 TGTTTCTGGAAGTTTGCTAGAAAAGGGAAGAAGGGAAAAAGAGATTAGTTATGTCCGACA 1399

Qy      1621 TTTGAAGCTGGA 1632
Db      1400 TTTGAAGCTGAA 1411
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RESULT 13
US-09-949-016-2735
; Sequence 2735, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2735
; LENGTH: 1323
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-2735

Query Match 55.0%; Score 941.8; DB 4; Length 1323;
Best Local Similarity 83.6%; Pred. No. 1e-266;
Matches 1104; Conservative 0; Mismatches 212; Indels 5; Gaps 3;

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Qy        11 ACCAGGATGACTCTGAAATGGACTTCAGTTCTTCTGCTGATACATCTCCAGTTGTTACTT 70
Db         5 ACCAGGATGTCTCTGAAATGGACGTCAGTCTTTCTGCTGATACAGCT-CAGTTGTTACTT 63

Qy        71 TAGCTCTGGGAGTTGTGGAAAAGTGCTGGTGTGGGCCGCAGAATACAGCCATTGGATGAA 130
Db        64 TAGCTCTGGAAGCTGTGGAAAGGTGCTAGTGTGGCCCACAGAATACAGCCATTGGATAAA 123

Qy       131 TATGAAGACAATCCTGAAAGAGCTTGTTCAGAGAGGTCATGAGGTGACTGTACTGGCATC 190
Db       124 TATGAAGACAATCCTGGAAGAGCTTGTTCAGAGGGGTCATGAGGTGACTGTGTTGACATC 183

Qy       191 TTCAGCTTCCATTCTTTTTGATCCCAATGATGCATCCACTCTTAAATTTGAAGTTTATCC 250
Db       184 TTCGGCTTCTACTCTTGTCAATGCCAGTAAATCATCTGCTATTAAATTAGAAGTTTATCC 243

Qy       251 TACATCTTTAACTAAAACTGAATTTGAGAATATCATCATGCAACAGGTTAAGAGATGG-- 308
Db       244 TACATCTTTAACTAAAAATTATTTGGAAGATTCTCTTCTGAAAATTCTCGATAGATGGAT 303

Qy       309 -TCAGACATTCGAAAAGATAGCTTTTGGTTATATTTTTCACAAGAACAAGAAATCCTGTG 367
Db       304 ATATGGTGTTTCAAAAAATACATTTTGGTCATATTTTTCACAATTACAAGAATTGTGTTG 363

Qy       368 GGAATTATATGACATATTTAGAAACTTCTGTAAAGATGTAGTTTCAAATAAGAAAGTTAT 427
Db       364 GGAATATTATGACTACAGTAACAAGCTCTGTAAAGATGCAGTTTTGAATAAGAAACTTAT 423

Qy       428 GAAAAAACTACAAGAGTCAAGATTTGACATCGTTTTTGCAGATGCTGTTTTTCCCTGTGG 487
Db       424 GATGAAACTACAAGAGTCAAAGTTTGATGTCATTCTGGCAGATGCCCTTAATCCCTGTGG 483
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Qy        488 TGAGCTGCTGGCTGCGCTACTTAACATACGGTTTGTGTACAGTCTCCGCTTTACTCCTGG 547
              |||||| |||||||  ||| |||||||||  ||| |||||||||| || ||  ||  |||
Db        484 TGAGCTACTGGCTGAACTATTTAACATACCCTTTCTGTACAGTCTTCGATTCTCTGTTGG 543

Qy        548 CTACACAATTGAAAGGCACAGTGGAGGACTGATTTTCCCTCCTTCCTACATACCTATTGT 607
              ||||||| |||| | | |  |||||||| |  | ||||||||||||||  ||||| ||||
Db        544 CTACACATTTGAGAAGAATGGTGGAGGATTTCTGTTCCCTCCTTCCTATGTACCTGTTGT 603

Qy        608 TATGTCAAAATTAAGTGATCAAATGACTTTCATGGAGAGGGTAAAAAATATGATCTATGT 667
              ||||||| |||||||||||||||||| |||||||||||| ||||||||||||  || |
Db        604 TATGTCAGAATTAAGTGATCAAATGATTTTCATGGAGAGGATAAAAAATATGATACATAT 663

Qy        668 GCTTTATTTTGACTTTTGGTTCCAAATGTCTGATATGAAGAAGTGGGATCAGTTTTACAG 727
              |||||||||||||||||||| ||||| | |||| |||||||||||| |||||||| ||
Db        664 GCTTTATTTTGACTTTTGGTTTCAAATTTATGATCTGAAGAAGTGGGACCAGTTTTATAG 723

Qy        728 TGAAGTTTTAGGAAGACCCACTACCTTATTTGAGACAATGGGAAAAGCTGACATATGGCT 787
              ||||||| |||||||||||||||| |||||||||||||||| |||||||| || |||||
Db        724 TGAAGTTCTAGGAAGACCCACTACATTATTTGAGACAATGGGGAAAGCTGAAATGTGGCT 783

Qy        788 TATGCGAAACTCCTGGAGTTTTCAATTTCCTCATCCATTCTTACCAAACGTTGATTTTGT 847
              || |||| ||  |||  |||| |||||||||  |||||||||||||| ||||||||||
Db        784 CATTCGAACCTATTGGGATTTTGAATTTCCTCGCCCATTCTTACCAAATGTTGATTTTGT 843

Qy        848 TGGAGGATTCCACTGGCAAACCTGCCAAACCCCTACCTAAGGAAATGGAGGAGTTTGTAC 907
              ||||||| | |||| | ||||| |||||||||| |||||||||||||| |||||||| |
Db        844 TGGAGGACTTCACT-GTAAACCAGCCAAACCCCTGCCTAAGGAAATGGAAGAGTTTGTGC 902

Qy        908 AGAGCTCTGGAGAAAATGGTGTTGTGGTGTTTTCTCTGGGGTCAGTGATAAGTAACATGA 967
              |||||||||||||||||||| |||||||||||||||||||||  |||| |||||||||
Db        903 AGAGCTCTGGAGAAAATGGTATTGTGGTGTTTTCTCTGGGGTCGATGATCAGTAACATGT 962

Qy        968 CAGCAGAAAGGGCCAATGTAATTGCAACAGCCCTTGCCAAGATCCCACAAAAGGTTCTGT 1027
              ||| |||||| |||||  | |||||| |||||||||| |||||||||||||||||||| |
Db        963 CAGAAGAAAGTGCCAACATGATTGCATCAGCCCTTGCCCAGATCCCACAAAAGGTTCTAT 1022

Qy       1028 GGAGATTTGATGGGAATAAACCAGATGCCTTAGGTCTCAATACTCGGCTGTATAAGTGGA 1087
              |||||||||||| || || ||| || | |||||| |||||||| ||||| ||||||
Db       1023 GGAGATTTGATGGCAAGAAGCCAAATACTTTAGGTTCCAATACTCGACTGTACAAGTGGT 1082

Qy       1088 TACCCCAGAATGACCTTCTAGGTCATCCAAAAACCAGAGCTTTTATAACTCATGGTGGAG 1147
              |||||||||||||||||| |||||||| ||||||| |||||||||||||||||||||||
Db       1083 TACCCCAGAATGACCTTCTTGGTCATCCCAAAACCAAAGCTTTTATAACTCATGGTGGAA 1142

Qy       1148 CCAATGGCATCTATGAGGCAATCTACCATGGGATCCCTATGGTGGGCATTCCATTGTTTT 1207
              |||||||||||||||||| |||||||||||||||||||||||||||||||||| ||||||
Db       1143 CCAATGGCATCTATGAGGCGATCTACCATGGGATCCCTATGGTGGGCATTCCCTTGTTTG 1202

Qy       1208 GGGATCAACCTGATAACATTGCTCACATGAAGGCCAAGGGAGCAGCTGTTAGATTGGACT 1267
               |||||||| |||||||||||||||||||| |||||||||||||| | ||  |||||
Db       1203 CGGATCAACATGATAACATTGCTCACATGAAAGCCAAGGGAGCAGCCCTCAGTGTGGACA 1262

Qy       1268 TCAACACAATGTCGAGTACAGACCTGCTGAATGCACTGAAGACAGTAATTAATGATCCTT 1327
              |||  || ||||| |||| |||  |||| |||||| ||||| |||| |||||||| |||
Db       1263 TCAGGACCATGTCAAGTAGAGATTTGCTCAATGCATTGAAGTCAGTCATTAATGACCCTG 1322

Qy       1328 T 1328
              |
Db       1323 T 1323
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RESULT 14
US-09-949-016-2736
; Sequence 2736, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
;  APPLICANT: VENTER, J. Craig et al.
;  TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
;  TITLE OF INVENTION:  WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001307
;  CURRENT APPLICATION NUMBER: US/09/949,016
;  CURRENT FILING DATE:  2000-04-14
;  PRIOR APPLICATION NUMBER: 60/241,755
;  PRIOR FILING DATE: 2000-10-20
;  PRIOR APPLICATION NUMBER: 60/237,768
;  PRIOR FILING DATE: 2000-10-03
;  PRIOR APPLICATION NUMBER: 60/231,498
;  PRIOR FILING DATE: 2000-09-08
;  NUMBER OF SEQ ID NOS: 207012
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2736
;   LENGTH: 1323
;   TYPE: DNA
;   ORGANISM: Human
US-09-949-016-2736

  Query Match             55.0%;  Score 941.8;  DB 4;  Length 1323;
  Best Local Similarity   83.6%;  Pred. No. 1e-266;
  Matches 1104;  Conservative    0;  Mismatches  212;  Indels    5;  Gaps    3;

Qy         11 ACCAGGATGACTCTGAAATGGACTTCAGTTCTTCTGCTGATACATCTCCAGTTGTTACTT 70
              |||||||| |||||||||||||| |||||  |||||||||||||| || ||||||||||
Db          5 ACCAGGATGTCTCTGAAATGGACGTCAGTCTTTCTGCTGATACAGCT-CAGTTGTTACTT 63

Qy         71 TAGCTCTGGGAGTTGTGGAAAAGTGCTGGTGTGGGCCGCAGAATACAGCCATTGGATGAA 130
              ||||||||| || |||||||| ||||| |||||| || |||||||||||||||||||| ||
Db         64 TAGCTCTGGAAGCTGTGGAAAGGTGCTAGTGTGGCCCACAGAATACAGCCATTGGATAAA 123

Qy        131 TATGAAGACAATCCTGAAAGAGCTTGTTCAGAGAGGTCATGAGGTGACTGTACTGGCATC 190
              |||||||||||||||| |||||||||||||||| |||||||||||||||||  || ||||
Db        124 TATGAAGACAATCCTGGAAGAGCTTGTTCAGAGGGGTCATGAGGTGACTGTGTTGACATC 183

Qy        191 TTCAGCTTCCATTCTTTTTGATCCCAATGATGCATCCACTCTTAAATTTGAAGTTTATCC 250
              ||| ||||| | |||| |  || ||| | |  ||||  || |||||| ||||||||||
Db        184 TTCGGCTTCTACTCTTGTCAATGCCAGTAAATCATCTGCTATTAAATTAGAAGTTTATCC 243

Qy        251 TACATCTTTAACTAAAACTGAATTTGAGAATATCATCATGCAACAGGTTAAGAGATGG-- 308
              ||||||||||||||||| | | || ||  ||    || ||     | | ||||||
Db        244 TACATCTTTAACTAAAAATTATTTGGAAGATTCTCTTCTGAAAATTCTCGATAGATGGAT 303

Qy        309 -TCAGACATTCGAAAAGATAGCTTTTGGTTATATTTTTCACAAGAACAAGAAATCCTGTG 367
               |  |  ||  |||| |||  ||||||| |||||||||||||  ||||||| |    ||
Db        304 ATATGGTGTTTCAAAAAATACATTTTGGTCATATTTTTCACAATTACAAGAATTGTGTTG 363

Qy        368 GGAATTATATGACATATTTAGAAACTTCTGTAAAGATGTAGTTTCAAATAAGAAAGTTAT 427
              |||||  ||||||      ||  ||  |||||||||||| |||||  |||||||| ||||
Db        364 GGAATATTATGACTACAGTAACAAGCTCTGTAAAGATGCAGTTTTGAATAAGAAACTTAT 423

Qy        428 GAAAAAACTACAAGAGTCAAGATTTGACATCGTTTTTGCAGATGCTGTTTTTCCCTGTGG 487
              ||  |||||||||||||||  |||||  || || | ||||||||  ||  |||||||||
Db        424 GATGAAACTACAAGAGTCAAAGTTTGATGTCATTCTGGCAGATGCCCTTAATCCCTGTGG 483

Qy        488 TGAGCTGCTGGCTGCGCTACTTAACATACGGTTTGTGTACAGTCTCCGCTTTACTCCTGG 547
              |||||| |||||||  ||| |||||||||  ||| |||||||||| || ||  ||  |||
Db        484 TGAGCTACTGGCTGAACTATTTAACATACCCTTTCTGTACAGTCTTCGATTCTCTGTTGG 543

Qy        548 CTACACAATTGAAAGGCACAGTGGAGGACTGATTTTCCCTCCTTCCTACATACCTATTGT 607
              ||||||| |||| | | |  |||||||| |  | ||||||||||||||  ||||| ||||
Db        544 CTACACATTTGAGAAGAATGGTGGAGGATTTCTGTTCCCTCCTTCCTATGTACCTGTTGT 603

Qy        608 TATGTCAAAATTAAGTGATCAAATGACTTTCATGGAGAGGGTAAAAAATATGATCTATGT 667
              ||||||| |||||||||||||||||| |||||||||||| ||||||||||||  || |
Db        604 TATGTCAGAATTAAGTGATCAAATGATTTTCATGGAGAGGATAAAAAATATGATACATAT 663

Qy        668 GCTTTATTTTGACTTTTGGTTCCAAATGTCTGATATGAAGAAGTGGGATCAGTTTTACAG 727
              |||||||||||||||||||| ||||| | |||| |||||||||||| |||||||| ||
Db        664 GCTTTATTTTGACTTTTGGTTTCAAATTTATGATCTGAAGAAGTGGGACCAGTTTTATAG 723

Qy        728 TGAAGTTTTAGGAAGACCCACTACCTTATTTGAGACAATGGGAAAAGCTGACATATGGCT 787
              ||||||| |||||||||||||||| |||||||||||||||| |||||||| || |||||
Db        724 TGAAGTTCTAGGAAGACCCACTACATTATTTGAGACAATGGGGAAAGCTGAAATGTGGCT 783

Qy        788 TATGCGAAACTCCTGGAGTTTTCAATTTCCTCATCCATTCTTACCAAACGTTGATTTTGT 847
              || |||| ||  |||  |||| |||||||||  |||||||||||||| ||||||||||
Db        784 CATTCGAACCTATTGGGATTTTGAATTTCCTCGCCCATTCTTACCAAATGTTGATTTTGT 843
```

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Qy        848 TGGAGGATTCCACTGGCAAACCTGCCAAACCCCTACCTAAGGAAATGGAGGAGTTTGTAC 907
Db        844 TGGAGGACTTCACT-GTAAACCAGCCAAACCCCTGCCTAAGGAAATGGAAGAGTTTGTGC 902

Qy        908 AGAGCTCTGGAGAAAATGGTGTTGTGGTGTTTTCTCTGGGGTCAGTGATAAGTAACATGA 967
Db        903 AGAGCTCTGGAGAAAATGGTATTGTGGTGTTTTCTCTGGGGTCGATGATCAGTAACATGT 962

Qy        968 CAGCAGAAAGGGCCAATGTAATTGCAACAGCCCTTGCCAAGATCCCACAAAAGGTTCTGT 1027
Db        963 CAGAAGAAAGTGCCAACATGATTGCATCAGCCCTTGCCCAGATCCCACAAAAGGTTCTAT 1022

Qy       1028 GGAGATTTGATGGGAATAAACCAGATGCCTTAGGTCTCAATACTCGGCTGTATAAGTGGA 1087
Db       1023 GGAGATTTGATGGCAAGAAGCCAAATACTTTAGGTTCCAATACTCGACTGTACAAGTGGT 1082

Qy       1088 TACCCCAGAATGACCTTCTAGGTCATCCAAAAACCAGAGCTTTTATAACTCATGGTGGAG 1147
Db       1083 TACCCCAGAATGACCTTCTTGGTCATCCCAAAACCAAAGCTTTTATAACTCATGGTGGAA 1142

Qy       1148 CCAATGGCATCTATGAGGCAATCTACCATGGGATCCCTATGGTGGGCATTCCATTGTTTT 1207
Db       1143 CCAATGGCATCTATGAGGCGATCTACCATGGGATCCCTATGGTGGGCATTCCCTTGTTTG 1202

Qy       1208 GGGATCAACCTGATAACATTGCTCACATGAAGGCCAAGGGAGCAGCTGTTAGATTGGACT 1267
Db       1203 CGGATCAACATGATAACATTGCTCACATGAAAGCCAAGGGAGCAGCCCTCAGTGTGGACA 1262

Qy       1268 TCAACACAATGTCGAGTACAGACCTGCTGAATGCACTGAAGACAGTAATTAATGATCCTT 1327
Db       1263 TCAGGACCATGTCAAGTAGAGATTTGCTCAATGCATTGAAGTCAGTCATTAATGACCCTG 1322

Qy       1328 T 1328
Db       1323 T 1323
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RESULT 15
US-09-976-594-241
; Sequence 241, Application US/09976594
; Patent No. 6673549
; GENERAL INFORMATION:
; APPLICANT: Furness, Michael
; APPLICANT: Buchbinder, Jenny
; TITLE OF INVENTION: GENES EXPRESSED IN C3A LIVER CELL CULTURES TREATED WITH STEROIDS
; FILE REFERENCE: PA-0041 US
; CURRENT APPLICATION NUMBER: US/09/976,594
; CURRENT FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: 60/240,409
; PRIOR FILING DATE: 2000-10-12
; NUMBER OF SEQ ID NOS: 1143
; SOFTWARE: PERL Program
; SEQ ID NO 241
; LENGTH: 2966
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No. 6673549 997080.1
US-09-976-594-241

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  Query Match             43.4%;  Score 742.8;  DB 4;  Length 2966;
  Best Local Similarity   68.3%;  Pred. No. 6.7e-208;
  Matches 1056;  Conservative    0;  Mismatches  483;  Indels    7;  Gaps    2;

Qy         70 TTAGCTCTGGGAGTTGTGGAAAAGTGCTGGTGTGGGCCGCAGAATACAGCCATTGGATGA 129
Db         82 TTGGCTGTGGATTCTGTGGGAAAGTCCTGGTGTGGCCCTGTGACATGAGCCATTGGCTTA 141

Qy        130 ATATGAAGACAATCCTGAAAGAGCTTGTTCAGAGAGGTCATGAGGTGACTGTACTGGCAT 189
Db        142 ATGTCAAGGTCATTCTAGAAGAGCTCATAGTGAGAGGCCATGAGGTAACAGTATTGACTC 201

Qy        190 CTTCAGCTTCCATTCTTTTTGATCCCAATGATGCATCCACTCTTAAATTTGAAGTTTATC 249
Db        202 ACTCAAAGCCTTCGTTAATTGACTACAGGAAGCCTTCTGCATTGAAATTTGAGGTGGTCC 261

Qy        250 CTACATCTTTAACTAAAACTGAATTTGAGAATATCATCATGCAACAGGTTAAGAGATGGT 309
Db        262 ATATGCCACAGGACAGAACAGAAGAAAATGAAATATTTGTTGACCTAGCTCTGA------ 315

Qy        310 CAGACATTCGAAAAGATAGCTTTTGGTTATATTTTCACAAGAACAAGAAATCCTGTGGG 369
Db        316 ATGTCTTGCCAGGCTTATCAACCTGGCAATCAGTTATAAAATTAAATGATTTTTTTGTTG 375

Qy        370 AATTATATGACATATTTAGAAACTTCTGTAAAGATGTAGTTTCAAATAAGAAAGTTATGA 429
Db        376 AAATAAGAGGAACTTTAAAAATGATGTGTGAGAGCTTTATCTACAATCAGACGCTTATGA 435

Qy        430 AAAAACTACAAGAGTCAAGATTTGACATCGTTTTTGCAGATGCTGTTTTTCCCTGTGGTG 489
Db        436 AGAAGCTACAGGAAACCAACTACGATGTAATGCTTATAGACCCTGTGATTCCCTGTGGAG 495

Qy        490 AGCTGCTGGCTGCGCTACTTAACATACGGTTTGTGTACAGTCTCCGCTTTACTCCTGGCT 549
Db        496 ACCTGATGGCTGAGTTGCTTGCAGTCCCTTTTGTGCTCACACTTAGAATTTCTGTAGGAG 555

Qy        550 ACACAATTGAAAGGCACAGTGGAGGACTGATTTTCCCTCCTTCCTACATACCTATTGTTA 609
Db        556 GCAATATGGAGCGAAGCTGTGGGAAACTTCCAGCTCCACTTTCCTATGTACCTGTGCCTA 615

Qy        610 TGTCAAAATTAAGTGATCAAATGACTTTCATGGAGAGGGTAAAAAATATGATCTATGTGC 669
Db        616 TGACAGGACTAACAGACAGAATGACCTTTCTGGAAAGAGTAAAAAATTCAATGCTTTCAG 675

Qy        670 TTTATTTTGACTTTTGGTTCCAAATGTCTGATATGAAGAAGTGGGATCAGTTTTACAGTG 729
Db        676 TTTTGTTCCACTTCTGGATTCAGGATTACGACTATCATTTTTGGGAAGAGTTTTATAGTA 735

Qy        730 AAGTTTTAGGAAGACCCACTACCTTATTTGAGACAATGGGAAAAGCTGACATATGGCTTA 789
Db        736 AGGCATTAGGAAGGCCCACTACATTATGTGAGACTGTGGGAAAAGCTGAGATATGGCTAA 795

Qy        790 TGCGAAACTCCTGGAGTTTTCAATTTCCTCATCCATTCTTACCAAACGTTGATTTTGTTG 849
Db        796 TACGAACATATTGGGATTTTGAATTTCCTCAACCATACCAACCTAACTTTGAGTTTGTTG 855

Qy        850 GAGGATTCCACTGGCAAACCTGCCAAACCCCTACCTAAGGAAATGGAGGAGTTTGTACAG 909
Db        856 GAGGATTGCACT-GTAAACCTGCCAAAGCTTTGCCTAAGGAAATGGAAAATTTTGTCCAG 914

Qy        910 AGCTCTGGAGAAAATGGTGTTGTGGTGTTTTCTCTGGGGTCAGTGATAAGTAACATGACA 969
Db        915 AGTTCAGGGGAAGATGGTATTGTGGTGTTTTCTCTGGGGTCACTGTTTCAAAATGTTACA 974

Qy        970 GCAGAAAGGGCCAATGTAATTGCAACAGCCCTTGCCAAGATCCCACAAAAGGTTCTGTGG 1029
Db        975 GAAGAAAAGGCTAATATCATTGCTTCAGCCCTTGCCCAGATCCCACAGAAGGTGTTATGG 1034

Qy       1030 AGATTTGATGGGAATAAACCAGATGCCTTAGGTCTCAATACTCGGCTGTATAAGTGGATA 1089
Db       1035 AGGTACAAAGGAAAAAAACCATCCACATTAGGAGCCAATACTCGGCTGTATGATTGGATA 1094

Qy       1090 CCCCAGAATGACCTTCTAGGTCATCCAAAAACCAGAGCTTTTATAACTCATGGTGGAGCC 1149
Db       1095 CCCCAGAATGATCTTCTTGGTCATCCCAAAACCAAAGCTTTTATCACTCATGGTGGAATG 1154

Qy       1150 AATGGCATCTATGAGGCAATCTACCATGGGATCCCTATGGTGGGCATTCCATTGTTTTGG 1209
Db       1155 AATGGGATCTATGAAGCTATTTACCATGGGGTCCCTATGGTGGGAGTTCCCATATTTGGT 1214

Qy       1210 GATCAACCTGATAACATTGCTCACATGAAGGCCAAGGGAGCAGCTGTTAGATTGGACTTC 1269
Db       1215 GATCAGCTTGATAACATAGCTCACATGAAGGCCAAAGGAGCAGCTGTAGAAATAAACTTC 1274
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Qy       1270 AACACAATGTCGAGTACAGACCTGCTGAATGCACTGAAGACAGTAATTAATGATCCTTTA 1329
              || || ||| | ||   |||  | ||||  ||  |||  ||||| ||||  ||| | |
Db       1275 AAAACTATGACAAGCGAAGATTTACTGAGGGCTTTGAGAACAGTCATTACCGATTCCTCT 1334

Qy       1330 TATAAAGAGAATATTATGAAATTATCAAGAATTCAACATGATCAACCAGTAAAGCCCCTG 1389
              |||||||||||  ||||| ||||||||||||||| |||||||||| ||||||||||
Db       1335 TATAAAGAGAATGCTATGAGATTATCAAGAATTCACCATGATCAACCTGTAAAGCCCCTA 1394

Qy       1390 GATCGAGCAGTCTTCTGGATTGAATTTGTCATGCCCCACAAAGGAGCCAAACACCTTCGA 1449
              |||||||||||||||||| || |||||||||| |||||||||||||| ||||| |||
Db       1395 GATCGAGCAGTCTTCTGGATCGAGTTTGTCATGCGCCACAAAGGAGCCAAGCACCTGCGA 1454

Qy       1450 GTTGCAGCCCATGACCTCACCTGGTTCCAGTACCACTCTTTGGATGTGATTGGGTTTCTG 1509
                || ||||||||||||||||||||||| || ||||| | |||||||||||||| |||
Db       1455 TCAGCTGCCCATGACCTCACCTGGTTCCAGCACTACTCTATAGATGTGATTGGGTTCCTG 1514

Qy       1510 CTGGCCTGTGTGGCAACTGTGATATTTATCATCACAAAGTTTTGTCTGTTTTGTTTCTGG 1569
              ||| |||||||||||||  ||||| |  |||||||| | || | | ||||  |
Db       1515 CTGACCTGTGTGGCAACTGCTATATTCTTGTTCACAAAATGTTTTTTATTTTCCTGTCAA 1574

Qy       1570 AAGTTTGCTAGAAAAGGGAAGAAGGGAAAAAGAGATTAGTTATGTC 1615
              || |||  || ||   | ||||  | ||| || || ||| | | ||
Db       1575 AAATTTAATAAAACTAGAAAGATAGAAAAGAGGGAATAGATCTTTC 1620
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Search completed: September 3, 2005, 09:18:01
Job time : 340 secs